1)5/01 Hitra R. 11/5/01 +WO 10/846060 Page 1

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OM nucleic - nucleic search, using sw model

Run on:

May 12, 2006, 16:33:29; Search time 15352 Seconds (without alignments) 11407.939 Million cell updates/sec

US-10-840-060-142 3081 1 aaactaaaaaattgtgttgc.....gccgaatggcaagcgttagt 3081 Title: Perfect score:

Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

5883141 segs, 28421725653 residues Searched:

Total number of hits satisfying chosen parameters:

11766282

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	C0573345 Sequence	AX777288 Sequence	AY051763 Drosophil	CQ573344 Seguence	AC017670 Drosophil	AC104510 Drosophil	AE003485 Drosophil	AC116537 Drosophil	AC007521 Drosophil	AC007521 Drosophil	BT001278 Drosophil	CQ577533 Sequence	CQ577532 Sequence	AC006245 Drosophil	AC099036 Drosophil	AE003459 Drosophil	AC013192 Drosophil	CQ578232 Sequence
SUMMARIES	ID	CQ573345	AX777288	AY051763	CQ573344	AC017670	AC104510	AE003485	AC116537	AC007521	AC007521	BT001278	CQ577533	CQ577532	AC006245	AC099036	AE003459	AC013192	CQ578232
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ALIGNMENTS

RESULT 1 COS 73345 COUS DETINITION ACCESSION VERSTON KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL	CQ573345 Sequence 1103 from Patent W00171042. CQ573345 CQ573345.1 GI:41637543 Drosophila sp. Dro
FEATURES source ORIGIN	Location/Qualifiers 13081 /organ="Drosophila sp." /mol_type="unassigned DNA" /db_xref="taxon:7242"
Query Match Best Local Sim Matches 3081;	Query Match 100.0%; Score 3081; DB 6; Length 3081; Best Local Similarity 100.0%; Pred. No. 0; Matches 3081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	1 AAACTAAAAAATTGTGTTGCTGACATCTGGTCGCTTGCAAAACTATTTCTAGCAGATTTT 60
4 4	61 GTGATATTTCGTTGTGATCGGTCGATAAATCCGCCAGTTTTTTTT
1 1	121 AACACATTGTAGCGGTTGGGAAGATAGCAGGAAAGAGCCAGCGGGGGGCTGCCGTTTTTCCTT 180

	CAGTOTGCCAAGCGTCCCATTAGCCGCCAAGAGGTCAATCGCAAGGAGATCGATC	1621 TCACCAAGTTCCTGGAGAACCACAAGTTTCGCTTCGACTACGCCTTCAACGACACGTGGG 1680 1621 TCACCAAGTTCCTGGAGAACCACAAGTTTCGCTTCGACTACGCCTTCAACGACACGTGGG 1680 1681 ACAATGCCATGGTATACAAATACACAGCCATGGTGAAAACCATTTTCGAGGGC 1740 1681 ACAATGCCATGGTATACAAATACACAGCCAAGCCGTTGGTGAAAACCATTTTCGAGGGC 1740 1681 ACAATGCCATGGTATACAAATACACAGCCGTTGGTGAAAACGCATTTTCGAGGGC 1740 1741 GAATGGCCATGGTATACAAATACACAGCCGAACGGCAAAACGCAAAACGCACATGGGCG 1800		1861 ATGTCTTTGTGACCTGAATATGCCGCGTTACCGCCCATGAATCTAGTCGTCTCGGCCA 1920 1861 ATGTCTTTGTGACCCTGAATATGCCGCGTTACCGCCCATGAATCTAGTCGTCTCGGCCA 1920 1921 GTTCTTTGAGATTTACAGTGGCAAGGTCTTCGATCTTCTGTCCGACAAGCAGAAACTGC 1980 1921 GTTCTTTGAGATTTACAGTGGCAAGGTCTTCGATCTTCTGTCCGACAAGCAGAAACTGC 1980 1921 GTTCTTTGAGATTTACAGTGGCAAGGTCTTCGATCTTCTGTCCGACAAGCAGAAACTGC 1980	1981 GCGTCCTGGAGGATGGTAAACAGCAAGTGGTGGTGGTGGACTCACCGAGAAGGTGGTCG 2040 1981 GCGTCCTGGAGGATGGTAAACAGCAAGTGCAGGTGGTGGACTCACCGAGAAGGTGGTCG 2040 2041 ATGGCGTCGAGGAGGTACTGAAGGTCATCCAGCACGAGATGCTGCCGAACATCCGGC 2040 2041 ATGGCGTCGAGGAGGTACTCAAGCTCATCCAGCACAGATGCTGCCCGAACATCCGGCC 2100 2041 ATGGCGTCGAGGAGGTACTGAAGGTCATCCAGCACACAGCAGCCCCGAACATCCGGCC 2100	2101 AGACGTCGGCCAATTCGTCGCGTTCGCACGCCGTTTCCAGATTGTGCTGCGGC 2160		2281 AATGGCTGGTGGCCCTCAAGGAGTGCATTGGTGGGCTTGGGCAAACAGTCGGCCCACTTGC 2340 2341 CCTTCCGTGTCTCCAAACTCACCCAGGTGCTGGGGAACTCGTTCATTGGCGAGAAGAGA 2400 [
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181 TTTGTTATCGGTTGCCAGACGCAA 181 TTTGTTATCGGTTGCCAGACGCAA 241 ACACATACTAACGCCGACCCGCAA 241 ACACATACTAACGCCGACCCGCAA 301 AAAAAACAGACGCTGTCGCGCACCGCAA 301 AAAAAACAGACGCTGTCGGCGACC 301 AAAAAACAGACGCTGTCGGCGACC 301 CTTGAATTCGGTTCGGGCGACC	361 CTTGAATTCGGTTCGGGCTTAGT 421 TAAAATTATTTTCGACCTAAAAA 421 TAAAATTATTTTCGACCTAAAAAA 481 TAGGCACATTTGCACACCACAA		661 TCATGACATCATTACGGTGGGGC 	781 AGCGCGCGAAACGAACGGCAAGG 				1201 CCAGCGCGCAGCCAGTGCTGGTC 1261 AGGCAGCGGCGGCGCTAGTACCC

ORIGIN Query Match 100.0%; Score 3081; DB 6; Length 3081; Best Local Similarity 100.0%; Pred. No. 0; Matches 3081; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 AAACTAAAAATTGTGTTGCTGACATCTGGTCGCTTGCAAAACTATTTCTAGCAGATTTT 60 Db 1 AAACTAAAATTGTGTTGCTGACATCTGGTCGCTTGCAAACTATTTCTAGCAGATTTT 60	QY 61 GTGATATTTCGTTGTGATCGGTCGATAAATCCGCCAGTTTTTTTT	Qy 121 AACACATTGTAGCGGTTGGAAAGATAGCAGCAGCGGCTGCCGTTTTTCCTT 180 Db 121 AACACATTGTAGCGGTTGGGAAGATAGCAGGAAAGAGCCAGCGGGCTGCCGTTTTTCCTT 180	Qy 181 TTTGTTATCCGTTGCCAGACGCAAAACGACAGACAGTTGGCATTTGAATTCAGCACAAAC 240 Db 181 TTTGTTATCCGTTGCCAGACGAAACGACAACGACAGAACGACAGTTGGCATTTGAATTCAGCACAAAC 240	Oy 241 ACACATACTAACGCCGACCCGCAAGCAGCACACACACACA	Qy 301 AAAAACAGACGCTCCGCCACCTCGACAAGCAGTTGGGTTCGATTTAGTTGTTGC 360	Qy 361 CTTGAATTCGGTCTTAGTTTCCACAAGTTTATCGCTCGTCAAGAAACAACGAAA 420 Db 361 CTTGAATTCGGTTCGGGGCTTAGTTTCCACAAGTTTATCGCTCGTCAAGAACAACGAAA 420	Qy 421 TAAAATTATTTTCGACCTAAAAATCTGACTAAATTGTGTTTTTTGTTTTATGTATTTATT	QY 481 TAGGGACATTTTGCACACACACACGTAGTTACTACATCTACGACTTACGAACTCCTCCT 540 Db 481 TAGGCACATTTTGCACACACAACGTAGTTACTACATCTACGACTAACGGAACTCCTCCT 540	Qy 541 GCAAGCAGTAGAAGTTCCTGTCCATCAAGCAGTACTCGGAGTTAACGCAGGATAAGCCGG 600 bb 541 GCAAGCAGTGGAAGTTGCTGTCCATCAAGCAGTAACTCGGAGTTAACGCAGATAAGCCGG 600	Qy 601 GAGAAAGAGATCGGTGGAGAATAGAGATTAGAGGTGGAGTCAAAGAGGAAGGA	Qy 661 TCATGGACATGATTACGGTGGGGCACAGAGCTCAAGATCAAGCGGACGGA	QY 721 ACATGGCGGTGGTGGCGGTGATCCACCAGTCGGGCAAGTGCAATGGTACG 780 Db 721 ACATGGCCGTGGTGGCGGTGATCAACCAGTCGGGCAAGTGCATCACAGTCGAATGGTAG 780	Qy 781 AGCGCGGCGAAACGAAGGGCAAGGAGTAGAACTGGACGCCATACTCACGCTCAATCCGG 840 Db 781 AGCGCGCGAAACGAAGGACAAGAAGAGGAGTAGAACTGGACGCCATACTCACGCTCAATCCGG 840	Oy 841 AGCTAATGCAAGATACTGTCGAACACGCGCCCCGGGAGCCCAAGAAACAAGCCACG 900 Db 841 AGCTAATGCAAGATACTGTCGAACACGCGCCCCGGAGCCCAAGAAACAAGCCACG 900	901 CGCCGATGAACCTCTCGCGTAATCCCACAATCGGCTATCGGTGGCAATCTCACCAGCC 9 901 CGCCGATGAACCTCTCGCGTAATCCCACAAATCGGTTATCGGTGGCAATCAACAGCC 901 CGCCGATGAACTCTCCGCGTAATCCCACACAATCGGGTGGCGTGCCAATCACCAGCC 9	
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1080 OY 1080 Db 1140 OY 1200 Db	1200 1260 Qy 1260 Db 1320 Cy	1320 DS CS	1440 Db	1500 QY 1560 DD		1680 QY 1680 Db	1740 Db 1740 QY 1800 Db	1860 QY 1860 Db	1920 QY 1920 Db	1980 QY 1980 Db	2040 QY 2040 Db	2100 RE AY 2100 LC DE
CGATTGTCAGCAGCAATAGCGTGAATACAAACCAACTCCAACACTACGGCCGGC	AACCC AACCC AACCC AACCC			GATCA CGATG CGATG	CGACC CGACC	TCACCAAGTTCCTGGAGAACCACAAGTTTCGCTTCGACTACGCCTTCAACGACACGTGCG	1681 ACANTGCCATGGTATACAAATACACGCCAAGCCGTTGGTGAAAACCATTTTGGAGGGCG 17 1681 ACANTGCTATACAACAGCCCAAGCCGTTGGTGAAAACCATTTTTGGAGGCG 17 1681 ACANTGCTATACAACAGCCCAAGCCGTGGTGAAAACCATTTTTGGAGGCG 17 1741 GAATGGCGACGTGCTTCGCCTACGCCAGACGGGATCGGGCAAAACGCAACACCATGGCG 18 1741 GAATGGCGACGTCTCGCCTACGCCTAAAACCCAAAACGCAAAACGCAACACACAAAAACAAAAAA	GTGAGTTTAATGGAAAGGTGCACGCTGCAAGAACGCATTCTACGCCGCCGCGCCAAGGGTTAATGGAAAAGGTGCAAGGCTTCAAGGCGCCATGGCGGCCCAAGGGTGCAAGAGTTAATGGAAAAGGTGCAAGAACGCAAGGCATCTAACGCAATGGCGAACGCCAAGG	1961 AIGTCTTTGTGACCCTGAATATGCCGCGTTACCGCGCCATGAATCTAGTCGTCTCGGCCA 19	1921 GTTTCTTTGAGATTTACAGTGGCAAGGTCTTCGATCTTCTGTCCGACAAGCAGAAACTGC 19 	1981 GCGTCCTGGAGGATGGTAAACAGCAAGTGCAGGTGGGGACTCACCGAGAAGGTGGTTCG 20	2041 ATGCCTCGAGGAGTACTGAAGCTCATCCAGCACAATGCTGCCCGAACATCCGGCC 21

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AL Submitted (10-AUG-2011) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, USA Sequence Submitted by:
Berkeley, CA 94720, USA Sequence Berkeley National Laboratory
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within 100 kb in the sequence thus we believe the sequence to reflect accurately this particular cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcription of unspliced precursor RNAs, and reverse transcription and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to contamped the sequences and relationship of Other sequences and email to contamped the sequences and email to sequences and enails of the sequences and emails of the sequences and emails to sequences and emails of the 
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                                                                                                               Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                            98 AGTITITITITATIGGAAAGTGCTAACACATTGTAGCGGTTGGGAAGATAGCAGGAAAG
                                                                                                                                                                GCACATTTTGCACACACACAACGTAGTTACTACATCTACGACTAACGGAACTCCTCCTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    938 GAGCTGGCGGCGCTAGTACCCGGCGATCGCACTTGAAAGAGGTGGAGCGACTGAAGG
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        Length 3516;
                                        Indels
       DB 2;
                                      33;
     Score 2605.2;
Pred. No. 0;
0; Mismatches
 84.6%;
98.8%;
                                    Conservative
Query Match
Best Local Similarity
Matches 2625; Conser
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336 TTGGGTTCGATTTAGTTGTCAATGCCTTGAATTCGGTTCGGGGCTTAGTTTCCACAAGTT 395 2392 TTGGGTTCGATTTAGTTGTCAATGCCTTGAATTCGGTTCGGGGCTTAGTTTCCACAAGTT 2451 396 TAGGGTCGAAGAACAAGACGTTGGGTTCGGGGCTTAGTTTCCACAAGAT 2451 396 TATCGGTCGTCGAAGAACAAGAATAAAATTATTTTCGACCTAAAAAAT 455 2452 TATCGCTCGTCAAGAAACAAGAAAAAAATTATTTTCGACCTAAAAAATTCGACTAAAT 455 [136 TRAGGUGGACGARGAGACGACATGATTACOGTGGGGGCGCAGGCGTCAG 295

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Watington,S., Williams,G., Williamson,A., Walczyk,R., Wooden,S.,
Weinstock,G. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 168583)
Worley, K. C.
Direct Submission
Submitsed (13-DEC-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (01-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 168583)
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Submitted (07-JUN-2002) Human Genome Sequencing Center, Departmer
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
6 (bases I to 168583)
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Direct Submission
Submitted (13-JUN-2002) Human Genome Sequencing Center, Department
Submitted (13-JUN-2002) Human Genetice, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jun 7, 2002 this sequence version replaced gi:18463995.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                      CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                           gc-help@bcm.tmc.edu
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COMMENT

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

(More Acids Res. 25:3389-3402) similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

ANNOTATION OF FEATURES:

Peatures listing

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69529 TIGGGTTCGATTTAGTTGTCAATGCCTTGAATTCGGGTCGGGGCCTTAGTTTCCACAAGTT 69470
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http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
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QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 ACACACACTGGGACACTCGAAAAAAAAAAAAAACAGCGGCCTGTCGGCGACCTCGACAAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCGCTCGTCAAGAACAACGAAATAAAATTATTTTCGACCTAAAAATCTGACTAAAT
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                                                                                                                                                                                                                                                                                                       'note="Polymorphism between Baylor and Celera reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Polymorphism between Baylor and Celera reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Polymorphism between Baylor and Celera
                                                                                                                                                                                                                                                                                                                                                                       'note="Polymorphism between Baylor and Celera
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                                                                                                                                    1. .168583
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llarity 99.6%; Pred. No. 2.7e-286;
Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                    'note="Below phred 30 quality." /function="low quality"
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                                                                                                                                                                                                                                                                                                                                                                                                          function="polymorphic site"
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30060. .30064
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                                                                                                                                                                                                                                                                                                                                                         129996
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Brakaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Diptera; Brachycera; Muscomorpha; Ropptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Bubydroidea; Drosophila.

1 (bases I to 281075); Idae; Drosophila.

2 (bases I to 281075); Idae; Drosophila.

2 (beorge; R. J., Lewis, S. E., Kidardes; S., Ashburner M., Henderson; S.N., Sutton G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L. X., Banatiddes, P.G., Eaverer, E.G., Helt, G., Nelson, C.R., Gabor, G.L., Abril, J.F., Agbayan, J.R., Yandell, M.D., Bahang, O., Change, M., Peisiffer, B.D., Wan, H.J., Bans, A., Bars, B., Basu, A., Bara, H., Boyle, C., Baxer, E.G., Helt, G., Nelson, C.R., Gabor, G.L., Abril, J.F., Agbayan, M. R., An, H.J., Andrews, Pfannkoch, C., Baldwin, D., Balles, M., Beneos, V.V., Berman, B.P., Bhandari, D., Bolahdov, S., Beecon, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bolahdov, S., Beecon, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bolahdov, S., Davengort, L. B., Ditter, M., Cawley, S., Dankov, S., Davengort, L. B., Diet, S., M., Dodson, K., Doug, L.B., Downes, M., Dudson, K., Doug, L.B., Downes, M., Dieter, S., M., Barris, M., Harris, M., AE003485 2005 Drosophila melanogaster chromosome X, section 37 of 74 of the Celniker, S.E., Wheeler, D.A., Kronmiller, B., Carlson, J.W.,
Celniker, S.E., Wheeler, D.A., Kronmiller, B., Carlson, J.W.,
Halpern, A., Patel, S., Adams, M., Champe, M., Dugan, S.P., Frise, E.,
Hodgson, A., George, R.A., Hoskins, R.A., Laverry, T., Muzny, D.M.,
Nelson, C.R., Pacleb, J.M., Park, S., Pfeiffer, B.D., Richards, S.,
Sodergren, B.J., Svirskas, R., Tabor, P.E., Wan, K., Stapleton, M.,
Sutton, G.G., Venter, C., Weinstock, G., Scherer, S.E., Myers, E.W.,
Gibbs, R.A. and Rubin, G.M.

Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence Genome Biol. 3 (12), RESEARCH0079 (2002)

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                                                                                                                                                                                                                                                                  5 (bases 1 to 283075)
Celniker, S., Carlson, J., Wan, K., Pfeiffer, B., Frise, E., George, R., Moskins, R., Stapleton, M., Pacleb, J., Park, S., Svirskas, R., Smith, E., Yu, C. and Rubin, G. Berkeley Drosophila Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                           6 (bases 1 to 283075)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
Annotation of the Drosophila melanogaster euchromatic genome: a systematic review
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (22-UUL-2005) FlyBase, Harvard University, Biological
Laboratories, 16 Divinity Ave, Cambridge, MA 02138, USA
On Sep 13, 2002 this sequence version replaced gi:10728182.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="FLYBASE:FBgn0030263"
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                                                                                                          Kaminker, J.S., Bergman, C.M., Kronmiller, B., Carlson, J., Sytrakkas, R., Patel, S., Frise, E., Wheeler, D.A., Lewis, S.E., Rubin, G.M., Ashburner, M. and Celniker, S.E.
The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective Genome Biol. 3 (12), RESEARCH0084 (2002)
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                                                                                          (bases 1 to 283075)
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CONSRTM
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Db 48642 ACGGCGAAATGATACGCGAAGCACGCTGGAATTTGTGCCGCTGCTCGATGGC 48583	ACTIGGSS ACTIGGSS ACTIGGS BY DAY linear HTG 18-MAY 2002 LOCUS ACTIGGSS ACTIGGSS ACTIGGS BY HTGG ACTIVEFIN. ACCESSION ACTIGGSS ACTIGGS HARD ACTIVE ACTIVE ACTIVE ACTIVE ACCESSION ACTIGGS HARD ACTIGGS HARD ACTIVE ACTIV
	615 TACAGGTGGAGTCAAAGAGATCATGGACATCATTACGGTGGGCAAGGCTCAAGG 49122

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218063 ACACACACTGGGACACTCGAAAAAAAAAAAGGGCGGTGTCGGCGACCTCGACAAGCAG 218122
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                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                          Submitted (29-MAR-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2752 contig of 2752 bp in length 2753 gap of unknown length 9885 9844; gap of unknown length 9885 13752; contig of 6632 bp in length 9585 13752; contig of 4168 bp in length 9585 13752; contig of 4168 bp in length 3753 13852; gap of unknown length 13852; gap of unknown length 13899; gap of unknown length 67745 45844; gap of unknown length 15845 5932; contig of 13788 bp in length 5845 13893; contig of 13788 bp in length 15845 13893; contig of 21199 bp in length 15845 13893; contig of 21199 bp in length 15845 13842; gap of unknown length 15849 104548; gap of unknown length 15849 104548; gap of unknown length 15849 104548; gap of unknown length 15841 123941; gap of unknown length 15842 123941; gap of unknown length 15862 183677; gap of unknown length 15863 18377; gap of unknown length 15863 1378 13777; gap of unknown length 15878 13777; gap of unknown length 15878 134028; contig of 51052 bp in length 15828 134028; contig of 65501 bp in length 15828 134028; contig of 65501 bp in length 15828 134028; contig of 65501 bp in length 15838
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to 1070 bp in length
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of 1039 bp in length
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f unknown length
of 8298 bp in length
unknown length
                   in length
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of 1156 bp in length
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of 1451 bp in length
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f unknown length
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Drosophila melanogaster BAC library, partial EcoRI in
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Pred. No. 9.2e-204;
0; Mismatches 84; Indels 1; Ga
19 169748: contig of 740 bp in length
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29 170620: contig of 332 bp in length
29 170927: contig of 237 bp in length
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30 17169: contig of 762 bp in length
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31 172527: gap of unknown length
31 172527: gap of unknown length
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32 172672: gap of unknown length
33 172672: gap of unknown length
34 175301: contig of 465 bp in length
36 175301: contig of 465 bp in length
37 176376: contig of 465 bp in length
37 176376: contig of 463 bp in length
37 17639: contig of 483 bp in length
37 17639: contig of 530 bp in length
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39 17629: gap of unknown length
31 17639: contig of 530 bp in length
31 17639: contig of 530 bp in length
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341 178549: contig of 609 bp in length
350 178249: contig of 619 bp in length
351 17823: gap of unknown length
352 17823: gap of unknown length
353 18628: gap of unknown length
361 178240: gap of unknown length
362 18023: contig of 636 bp in length
363 18023: contig of 636 bp in length
364 178940: gap of unknown length
365 18023: contig of 636 bp in length
367 18028: gap of unknown length
368 17840: gap of unknown length
368 17890: contig of 636 bp in length
37 1600: contig of 636 bp in length
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38 17800: contig of 636 bp in length

    1. .180919
    /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strai="y; cn bw sp"
    /db xref="taxon;7227"
/chromosome="X"

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contig of 1867 bp in length
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of 339 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="BACR49A04 (D698) RPCI-98 49.A.4"
/clone lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI in
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18: contig of 740 bp in .....
28: gap of unknown length
.8: contig of 320 bp in length
.650: gap of unknown length
.72190: contig of 737 bp in length
.7220: gap of unknown length
.72313: gap of unknown length
.72313: gap of unknown length
.72313: gap of unknown length
.77311: gap of unknown length
.77312: gap of unknown length
.77312: gap of unknown length
.77312: gap of unknown length
.77536: gap of unknown length
.77536: gap of unknown length
.77539: gap of unknown length
.77539: gap of unknown length
.77539: gap of unknown length
.77529: gap of unknown length
.77740: gap of unknown 
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31.4%; Score 967.8; DB 14; Length 180919;
Best Local Similarity 87.0%; Pred. No. 5e-175;
Matches 1055; Conservative 0; Mismatches 82; Indels 76; G
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/estimated length=unknown
2042. .2121
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estimated_length=unknown
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Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley and Particular Laboratory, One Cyclotron Koad,
Berkeley and Particular Description and Description and
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/product="A107729p"
/product="A207729p"
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SRQSSHLPFRGSKLTQVLRDSFVGGKKNKTCMIAMISPSWGSVENTLATLRYADRVKE
LIAKEDEHLQSVEGDGEKSPDLNEBSEPEMMADEGDBEPEDEDNQHLTISSEBASSY
NINNSYDMSRHHTLAILGPSRNAVDLGVAEQHALLVENLETYAHNFRQLKTDKEIEQYT
QNSESALMKLLAMVNRTRDVTHNYNFQKLLKEENQNAYKKGELDESE"
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KFLEHHKFRFDYTFDEECSNALVYDHTARPLIRTMFEGGNATCFAYGQTGSGKTHTMG
GEFFGKVQDCGTGIYAMAARDVFEEVSRPEYRQMGAKITCSFFEIYGTKVFDLLLDNK
                                                                                                                                                                                             Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases I to 2518)

I (bases I to 2518)

I (champe, M., Broketein, P., Hong, L., Agbayani, A., Carlson, J., Champe, M., Champella, M., Champella, M., Champella, M., Champella, M., Champella, M., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M. and Celnikeri, S.

Direct Submission

Submitted (15-NOV-2002) Berkeley Drosophila Genome Project,
Lawrence Berkeley, National Laboratory, One Cyclotron Road,
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                                                                                                                                          Drosophila melanogaster
Bukaryota, Metazoa, Arthropoda, Hexapoda,
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                                                                                                         Drosophila melanogaster (fruit fly)
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/db_xref="taxon:7227"
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/gene="CG12192"
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                                                                CAĞİĞĞCAAGGIGAGIGAGACAACATACAACTIGGCATGATIATCATACTIAGCIGIATT
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and the same and t	2019 ATGGAAGGAATGACGATGACGAAGGAATGAAGCTCATCCAGAAGGC 2018 1392 GGCCTAACGAGAAGTACCCAAGTGAAGGATCAAGACTCATCCAGCACGGC 2018 2079 AATGCTGCCCGAACATCCGGCCAGACGTCGACCTCCAATTCGTCGCACGCC 1451 2079 AATGCTGCCCGAACATCCGGCCAGACGTCGACCTCCCATTCGTCCCAGCCC 1181 2139 GTTTTCCAGATTGTGCTGCGCCCAGACGCCAAGTCATCGCGCTTCCCAGCC 1511 2139 GTTTTCCAGATTGTGCTGCGCCGCAGGCTCGACGCCAAGTCATCGCTTCCTTC
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                        Venter, J.C., Adams, M., Li, P.W. and Myers, E.W.
Detection kits, such as mucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof Patent: WO 0171042-A 5290 27-SEP-2001;
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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CQ577532.1 GI:41640334
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     the following cutoffs: length >= 200 bases. Pl library location:
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(clone lib="Pl library, partial Sau3A in pAd108acBII"
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                           NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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589 668 gap of unknown length
669 1229: contig of 561 bp in length
1220 1309: gap of unknown length
1310 82269: contig of 80960 bp in length
1270 82269: contig of 80960 bp in length
1270 82848: contig of 535 bp in length
1285 82848: contig of 535 bp in length
1285 83522: contig of 568 bp in length
1231 836122: gap of unknown length
1231 84419: contig of 807 bp in length
120cation/Qualifiers
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68.1%; Pred. No. 1.1e-97;
tive 0; Mismatches 379; Indels
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| forganism="Drosophila melanogaster"
| forganism="genomic DNA"
| fetrain="y; cn bw sp"
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chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="59D1-59D2"
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Listan, L.L. and Rubin, G.M.

Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Jul 30, 1999 this sequence version replaced gi:5630026.

Por further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTGS; HTGS PHASE:

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Drosophila melanogaster

Busaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Busaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

E (bases 1 to 84419)

B (clniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciestolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, R.A., Hummasti, S. R., Karra, K., Kerrney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfelffer, B., Poon, L., Sequira, A., Sethi, H., Snir, B., P., L., L. and B., Lewiss, R.H., Weinburg, T., Zhang, R., Zieran, L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster strain y; cn bw sp chromosome 2 clone DS07831 (D467) map 59D1-59D2, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces.
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                                                                                                                                                                                                                                                                                                                   ATTCGTGCGTTGGGCAAACAGTCGGCCCACTTGCCCTTCCGTGTCTCCAAACTCACCCAG 2366
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CGTTCGCACGCCGTTTTCCAGATTGTGCTGCGGCCGCAGGGCTCGACGAAGATCCATGGC
                                                                                                                                                                                                                                                              2453 cGrcaaacrcGcArcGaGGGGGGGAGArCAAraarcrcrGcrGGCCCrcaaGGAGTGC
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                                                                                                      AAGTICTCGTICATCGATCIGGCGGCCAAIGAGCGGGGGGGGGCGIGGACACTICCTCGGCCGAI
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Unpublished
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AUTHORS
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JOURNAL
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AUTHORS
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Submitted (08-NOV-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US Sequence submitted by:

Sequence submitted by:

Berkeley Drosophila Genome Project
Lawrence Berkeley Inational Laboratory, MS 64-121
Berkeley CA 94720

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
McIntosh, T.C., Moy, M., Murphy, B., Natcei, B., Moshrefi, A.,
Rolleb, J., Paragas, V., Park, S., Patel, S., Feiffer, B.,
Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished

2 (bases 1 to 180361)

S (clniker, S., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,

Rolt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,

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Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,

Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,

Mintosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,

Pacleb, J., Paragas, V., Park, S., Patel, S., Petel, E., Bhouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,

Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,

Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Direct Submission
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Drolone lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
pBACG3.6)"
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|0976 GTTTCGACTACACGTTCGACGAGGAGTGCTCCAATGCGCTGGTCTACGATCACACTGCT 30917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACCGGCAAATGGGTGCCAAGATTACGTGCAGCTTCTTCGAAATCTATGGCACCAAGGTG 30677
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                                                                                     AAGCCGTTGGTGAAAACCATTTTCGAGGCGGAATGGCGACGTGCTTCGCCTACGGCCAG
                                                                                                                                                                        ACGGGATCGGGCAAACGCACACCATGGGCGGTGAGTTTAATGGAAAGGTGCAGGACTGC
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Drosophila melanogaster
Bukaryota; Metazog, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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2424 TCGCCGGGACTTAGCTCCTGCGAGCACACGCTCAACACGCTGTCGGATCGTGC 2483
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IDENTITY_NUC Gapop 10.0 , Gapext 1.0

4996997 segs, 3332346308 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn1980s:* N_Geneseq_21:* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Abl02575 Drosophil	Adk11353 Drosophil	Abl02574 Drosophil	Abl05367 Drosophil	Abl05366 Drosophil	Abl05833 Drosophil	Abl05832 Drosophil	Aad24080 Human mit	Ade10082 DNA encod	Ado52609 Human mit	Aad24083 Human mit	Adel0088 DNA encod	Ado52615 Human mit	Aad24086 Human mit	Adel0094 DNA encod	Ado52621 Human mit	Aas94953 Human DNA	Aad24081 Human mit	Adel0084 DNA encod
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ALIGNMENTS

Drosophila melanogaster expressed polynucleotide SEQ ID NO 2207. ABL02575 standard; cDNA; 3081 BP (first entry) 26-MAR-2002 ABL02575; RESULT 1
ABL02575
ABL

Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss. Drosophila melanogaster.

WO200171042-A2. 27-SEP-2001. 620/

23-MAR-2001; 2001WO-US009231.

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150.

(PEKE) PE CORP NY.

Venter JC, Adams M,

Myers EW;

Li PWD,

WPI; 2001-656860/75. P-PSDB; ABB58472.

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.

Claim 1; SEQ ID NO 2207; 21pp + Sequence Listing; English.

18 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention

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The invention relates to novel Drosophila species DNA sequences and their encoded proteins with their corresponding human homologues. The proteins or their encoding polymucleotides are useful in a method of prevention, treatment or diagnosis of a disease are useful in a method of prevention, treatment or diagnosis of a disease in an individual, and used to identify a substance capable of binding to the polypeptide or modulating comparison of the polypeptide comprising incubating the polypeptide. The compositions are administered to an individual in need of such treatment. The method of diagnosis, in which the presence or absence of a polymucleotide is detected in a biological sample, comprises brining the biological sample containing the nucleic acid such as DNA or contact with a probe comprising a fragment of at least 15 nucleotides of the polymucleotide, and detecting any duplex formed between the probe and nucleic acid in the sample. The method also comprises providing an antibody capable of binding to the polymeptide, incubating a biological sample with the antibody to allow the formation of an antibody-antigen complex, and determining whether antibody-antigen complex comprises unch as cancer. The antibody to allow the formation of an antibody-antigen complex, and determining whether antibody-antigen complex comprises and a cancer. The antibody to allow the formation of and/or regulating a cell division cycle function of a polypeptide and/or regulating and rheumatoid arthritis, and dermatological disorders such as sportasis, inflammatory, fungal, and parasitic disorders such as such as psortasis, inflammatory, fungal, and parasitic disorders such as psortasis, inflammatory, this sequence represents one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Drosophila polypeptides and polynucleotides, useful for diagnosing, preventing and/or treating disorders, such as cancer, glomerulonephritis, rheumatoid arthritis, psoriasis, malaria, emphysema and alopecia.
                                                                                                                                                                                                             antirheumatic; antiarthritic; dermatological; antipsoriatic; antiinflammatory; fungicide; gene therapy; Drosophila; diagnosis; cardiovascular disorder; autoimmune disease; glomerulonephritis; rheumatoid arthritis; dermatological disorder; psoriasis; inflammatory disorder; malaria; emphysema; alopecia.
                                                                                                                                                  Drosophila kinesin-like protein KIF2 homolog gene.
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27-NOV-2001; 2001GB-00028384
11-FEB-2002; 2002GB-00003185.
                    ADK11353 standard; DNA; 3081
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Sequence 3081 BP; 803 A; 817 C; 868 G; 593 T; 0 U; 0 Other;

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                                                       developmental biology; cell signalling; insecticide;
Drosophila melanogaster expressed polynucleotide SEQ ID NO 2204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8043 BP; 2238 A; 1932 C; 1813 G; 2060 T; 0 U; 0 Other;
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11-JUL-2000; 2000US-00614150
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pharmaceutical; gene; ss.
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P-PSDB; ABB58471.
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P-PSDB; ABB61264.
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3039 CACGAGCCGCGCAGCAAGGTCGACCTCACCAAGTTCCTGGAGAACCACAAGTTTCGCTTC 3098 1415 1416 ACGGCGCAAATGATACGCGAATATCAGAGCACGCTGGAATTTGTGCCGCT-----GCTC 1469 552 612 GACTACGCCTTCAACGACACGTGCGACAATGCCATGGTATACAAATACACAGCCAAGCC 1714 18 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA ABGA2072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell GTAGTGAGGGAGGTGAATCGCATGAAGGAGCAGAGGAAAGCGAAGGGTTCGCCAGGCG GAGATGAAGGAGAAGGTGGCGCTGATGAACCAGGATCCGGGCAATCCAAACTGGGAG GAACAGCTCCAGGAGGAAGGATGCACTGCGTCGCAATAATCCGGGGGAATCCCAACTGGGAG GCATTGAAAGAGGTGGAGCGACTGAAGGAGAATCGCGAGAAGCGACGCCCCGACAGGCC Gaps Drosophila melanogaster expressed polynucleotide SEQ ID NO 10583 developmental biology; cell signalling; insecticide, 12; Length 2190; Sequence 2190 BP; 586 A; 574 C; 626 G; 404 T; 0 U; 0 Other; Claim 1; SEQ ID NO 10583; 21pp + Sequence Listing; English. Indels at ftp.wipo.int/pub/published_pct_sequences

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                                                                                                                           CGTCCGTTGATCAGAACCATGTTCGAGGGCGCAATGCCACTTGTTTTCGCTTACGGACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signailing and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB27137-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1312 AGCGACTGAAGGAGAATCGCGAGAAGCGACGACGCCCGACAGGCCGAGATGAAGGAGGAGAAGA 1371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                               developmental biology; cell signalling; insecticide;
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melanogaster expressed polynucleotide
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Pred. No. 3.9e-119;
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        Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                New human MCAK (mitotic centromere-associated kinesin) protein useful in identifying agents for use in the treatment of cellular proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human MCAK (mitotic centromere-associated kinesin) protein, and its fragments that comprise a motor domain and directly or indirectly produce ADP or phosphate. The MCAK enzyme and its fragments are used in methods to identify compounds that modulate their activity. Modulators of MCAK are useful as therapeutic agents for treating cellular proliferation disorders such as cancer, hyperplasiss, restenosis, cardiac hypertrophy, immune disorders, inflammation, autoimmune disease, arthritis, graft rejection, inflammatory bowel disease. The present sequence is a human MCAK fragment encoding DNA
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arthritis; graft rejection; inflammatory bowel disease;
                                                                                                          /product= "MCAK enzyme fragment"
/transl_except= (pos:4. .5, aa:Arg)
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4.8e-106;
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llarity 62.6%; Pred. No. 4.8e
Conservative 0; Mismatches
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1. .1292
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1660 ACGCCTTCAACGACACGTGCGACAATGCCATGGTATACAAATACACAGCCAAGCCGTTGG 1719

Humbn; MCAK; mitotic centromere-associated kinesin; motor domain; cellular proliferation disorder; cancer; hyperplasia; restenosis; carpiac hypertrophy; immune disorder; inflammation; autoimmune disease;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding motor proteins, useful in identifying compounds for the treatment of cellular proliferation disorders, such as cancer, autoimmune disease, inflammatory bowel disease, arthritis, keloids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of polynucleotide sequences encoding fragments of human motor protein, mitotic centromere-associated kinesin (MCAK). The MCAK enzyme fragments have microtubulestimulated Arbase activity. The invention also discloses methods for the use of the motor protein fragments. The methods and compositions are useful for high throughput screening systems for identifying compounds useful in the treatment of cellular proliferation disorders, such as cancer, autoimmune disease, arthritis, inflammatory bowel disease, keloids, psoriasis and tumours. The present sequence encodes a human MCAK
                                                                                                                                                  nucleotide deletion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 TGAGAATGAAGAGAG-----CTCAGGAGTATGACAGTAGTTTTCCAAACTGGGAATTTG
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which alters the reading frame"
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Pred. No. 4.8
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P-PSDB; ADE10083.
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                                                                                   TGAAAACCATTTTCGAGGGGGGGAATGGCGACGTGCTTCGCCTACGGCCAGACGGATCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated microtubule motor protein useful for identifying candidate agent for treating cellular proliferative diseases such as cancer, hyperplasia or restenosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides novel mitotic centromere-associated kinesin (MCAK) polypeptides and their encoding polynucleotides. The invernion is useful for treating cellular proliferative diseases such as cancer, hyperplasia, restenosis, cardiac hypertrophy, immune disorders and inflammation. The invention also acts as a cytostatic and vasotropic agent. The present sequence is human mitotic centromere-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGAAGGAGAGAAGTGGCGCTGATGAACCAGGATCCGGGCAATCCAAACTGGGAGACGG
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TTGCATTTGATGAAACAGCTTCGAATGAAGTTGTCTACAGGTTCACAGCAAGGCCACTGG
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calac hypertrophy; immune disorder; inflammation; cytostatic;
outopic; therapy; human; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human MCAK (mitotic centromere-associated kinesin) protein, and its fragments that comprise a motor domain and directly or indirectly produce ADP or phosphate. The MCAK enzyme and its fragments are used in methods to identify compounds that modulate their activity. Modulators of MCAK are useful as therapeutic agents for treating cellular proliferation disorders such as cancer, hyperplasias, restenosis, cardiac hypertrophy, immune disorders, inflammation, autoimmune disease, arthritis, graft rejection, inflammation, disease. The present sequence is a human MCAK fragment encoding DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human MCAK (mitotic centromere-associated kinesin) protein useful identifying agents for use in the treatment of cellular proliferation
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/note= "Base G at this location is missing in the sequence shown as SEQ ID NO: 7 in sequence listing specification"
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  GCAAAACGCACACCATGGGCGGTGAGTTTAATGGAAAGGTGCAGGACTGCAAGAACGGCA
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P-PSDB; ADE10089.
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/note= "This codon has an apparent 1 nucleotide deletion
           GCAAAACGCACACCATGGGCGGTGAGTTTAATGGAAAGGTGCAGGACTGCAAGAACGGCA
                                       GCAAGACACATACTATGGGCGGAGACCTCTGGGAAAGCCCAGAATGCATCCAAAAGGGA
                                                                       TCTACGCCATGGCGGCCAAGGATGTCTTTGTGACCCTGAATATGCCGCGTTACCGCGCCA
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New nucleic acid encoding motor proteins, useful in identifying compounds for the treatment of cellular proliferation disorders, such as cancer, autoimmune disease, inflammatory bowel disease, arthritis, keloids and
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                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated microtubule motor protein useful for identifying candidate agent for treating cellular proliferative diseases such as cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides novel mitotic centromere-associated kinesin (MCAK) polypeptides and their encoding polynucleotides. The invettion is useful for treating cellular proliferative diseases such as cancer, hyperplasia, restenosis, cardiac hypertrophy, immune disorders and inflammation. The invention also acts as a cytostatic and vasotropic agent. The present sequence is human mitotic centromere-associated kinesin (MCAK) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 TIGCATTIGAIGAAACAGCTICGAAIGAAGTIGICTACAGGITICACAGCAAGGCCACTGG 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 454.6; DB 12; Length
Pred. No. 5e-106;
0; Mismatches 434; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; SEQ ID NO 7; 46pp; English
28-AUG-2003; 2003US-00651510
                                                                 2000US-00724215
2002US-00112432
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Local Similarity 62.6%;
hes 747; Conservative
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                                                                                                                                                                  CYTOKINETICS
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                                                                                                                                                                                                                                                                                                   WPI; 2004-389161/36
                                                                                                                                                                                                                                                                                                                                     P-PSDB; ADO52616
                                                                 28-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAATCGCAAGGAGATCGATGTCATTTCGCTGCCGCCAAGGACATGCTCATCGTGCACG 1599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACCCAAGTTGAAAGTGGACTTAACAAAGTATCTGGAGAACCAAGCATTCTGCTTTGACT 931
                                                                                                                                                                                                                                              The invention relates to human MCAK (mitotic centromere-associated kinesin) protein, and its fragments that comprise a motor domain and directly or indirectly produce ADP or phosphate. The MCAK enzyme and its fragments are used in methods to identify compounds that modulate their activity. Modulators of MCAK are useful as therapeutic agents for treating cellular proliferation disorders such as cancer, hyperplassiss, restenosis, cardiac hypertrophy, immune disorders, inflammation, autoimmune disease, arthritis, graft rejection, inflammatory bowel disease. The present sequence is a human MCAK fragment encoding DNA
                                                                                                                                            New human MCAK (mitotic centromere-associated kinesin) protein useful identifying agents for use in the treatment of cellular proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAAGGAGGAGAAGGTGGCGCTGATGAACCAGGATCCGGGCAATCCAAACTGGGAGACGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 454.6; DB 6;
Pred. No. 6.2e-106;
                                                                                                                                                                                                                 Fig 13; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.8%;
62.6%;
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Matches 747; Conservative
                     (CYTO-) CYTOKINETICS INC
                                                        Sakowicz
                                                                                         2002-089075/12
                                                                                                           P-PSDB; AAE14505
                                                                                                                                                                                                                 Disclosure;
                                                        Beraud C,
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luhar proliferation disorder; cancer; hyperplasia; restenosis;
diac hypertrophy; immune disorder; inflammation; autoimmune disease;
hafitis; graft rejection; inflammatory bowel disease; ds.
TCTATGCCATGGCCTCCCGGGACGTCTTCCTCCTGAAGAATCAACCCTGCTACCGGAAGT
                                  TGAATCTAGTCGTCTCGGCCAGTTTCTTTGAGATTTACAGTGGCAAGGTCTTCGATCTTC
                                                                     TGGGCCTGGAAGTCTATGTGACATTCTTCGAGATCTACAATGGGAAGCTGTTTGACCTGC
                                                                                                       TGTCCGACAAGCAGAAACTGCGCGTCCTGGAGGATGGTAAACAGCAAGTGCAGGTGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequences encoding fragments of human motor protein, mitoric centromere-
associated kinesin (MCAK). The MCAK enzyme fragments have microtubule-
stimulated ATPase activity. The invention also discloses methods for the
use of the motor protein fragments. The methods and compositions are
useful for high throughput screening systems for identifying compounds
useful in the treatment of cellular proliferation disorders, such as
cancer, autoimmune disease, arthritis, inflammatory bowel disease,
keloids, psoriasis and tumours. The present sequence encodes a human MCAK
New nucleic acid encoding motor proteins, useful in identifying compounds for the treatment of cellular proliferation disorders, such as cancer, autoimmune disease, inflammatory bowel disease, arthritis, keloids and
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Pred. No. 6.2
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ilarity 62.6%;
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CGTTCATTGGCGAGAAGACGCAGATGATAGCCATGATCTCGCCGGGACTTAGCT 2439

2320 1586 2380 1646 2440

1080 ATGCTGCCCGAACATCCGGCCAGACGTCGGCCAACTCCAATTCGTCGCGTTCGCACGCCG

.292 decrecadadearerderraaererderdardardreareadardardaredaeareddea 1351

2020 GACTCACCGAGAAGGTGGTCGATGGCGTCGAGGAGGTACTGAAGCTCATCCAGCACGGCA

Search completed: May 12, 2006, 21:31:17 Job time : 1779 secs

GenCore version 5.1.8 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

May 12, 2006, 21:18:27; Search time 2381 Seconds (without alignments) 10700.527 Million cell updates/sec Run on:

US-10-840-060-142 3081 Title: Perfect score: Sequence:

1 aaactaaaaaattgtgttgc.....gccgaatggcaagcgttagt 3081

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

9793542 segs, 4134689005 residues Searched:

19587084

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

•• Database

Published Applications NA Main:*

1: /cgn2 6/ptodata1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2 6/ptodata1/pubpna/USO9_PUBCOMB.seq:*
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10: /cgn2 6/ptodata1/pubpna/USIOB_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 142, App	Seguence 1103. Ap						Sequence 1, Appli	7	13,	W		6	77	710,	1158,	Sequence 174, App	179,		13	3104	Sequence 3737, Ap	Sequence 4185, Ap
ID	US-10-840-060-142	US-11-097-143-1103	US-11-097-143-1102	US-11-097-143-5291	US-11-097-143-5290	US-11-097-143-5990	US-11-097-143-5989	US-10-651-510-1	US-10-651-510-7	US-10-651-510-13	US-10-240-965-208	US-10-651-510-3	US-10-651-510-9	US-09-954-456-77	US-09-954-456-710	US-09-954-456-1158	US-09-960-253-174	US-09-960-253-179	US-09-849-602-5	US-10-651-510-15	US-10-843-641A-3104	US-10-843-641A-3737	US-10-843-641A-4185
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% Query Match	100.0	100.0	50.2	18.3	18.3	16.4	16.4	14.8	14.8	14.8	14.7	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6	14.6
Score	3081	3081	1547.8	564.6	564.6	505.8	505.8	454.6	454.6	454.6	453	449.8	449.8	449.8	449.8	449.8	449.8	449.8	449.8	449.8	449.8	449.8	449.8
Result No.	1	7	m	4	S	9	C 7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23

Sequence 1328, Ap Sequence 1328, Ap Sequence 486, App	Sequence 5182, Ap Sequence 134, App Sequence 5, Appli Sequence 11, Appl	1386 1830 87,	Sequence 4857, Ap Sequence 146, App Sequence 294, App Sequence 294, App	Sequence 294, App Sequence 293, App Sequence 293, App Sequence 293, App	1, Ap
US-10-172-118-1328 US-10-342-887-1328 US-10-733-878-486	1 US-10-723-860-5182 1 US-09-925-300-134 1 US-10-651-510-5 1 US-10-651-510-11	US-10-094-749-1386 US-09-954-456-1830 US-10-737-450-87	US-10-843-641A-4857 US-10-840-060-146 US-10-037-270-294 US-10-117-722-294	US-10-122-851-294 US-10-037-270-293 US-10-117-722-293 US-10-122-851-293	-3-7-
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2825 2825 2825	2892 2741 1088 1217	2296 2905 2905	2905 2905 4617 4617	4617 4503 4503 4503	1476 909 1032 1032
14.6 14.6	14.4 13.8 13.8	12.9	12.2.2	12.8	11.8 11.4 7.3 7.3
4449.8 449.8	4445.2 425.2 425.6 6.2 6.2 6.2 6.2	408.6 396.6 396.6	396.6 395.8 395.8	395.8 395 395	365 352 226.4 226.4
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ALIGNMENTS

	ő	09 J	09 1	120	120	180	180
	Gaps	AGALTT	AGATTTT	AAGTGCT	AGTGCT	TTCCT	TTCCTT
	3081;	CTAGC	CTAGC	VATGGA	ATGGA	SCCGTT	CCGTT
	Length 3081; Indels 0;	ACTATT	ACTATT	TTTTT	TTTTT	CGGGCTC	CGGGCTC
oteins	,0 0,	TTGCAAA	TTGCAAA	CAGTTT	CAGTTT	BAGCCAG	BAGCCAG
sion Pr 960 30		GGTCGC	GGTCGC	ATCCCC	ATCCGC	AGGAAA	AGGAAA
Ublication No. US20050227243A1 Mublication No. US20050227243A1 APPLICANT: Deak, Peter APPLICANT: Deak, Peter APPLICANT: Deak, Peter APPLICANT: Glover, David APPLICANT: Glover, David APPLICANT: Midgley, Carol TITLE OF INVENTION: Cell Cycle Progression Proteins FILLE REFERENCE: 10069/2012 CURRENT APPLICANTON NUMBER: US/10/840,060 CURRENT FILING DATE: 2004-05-05 PRIOR FILING DATE: 2002-10-23 PRIOR PLICATION NUMBER: GB 0126506.5 PRIOR PLICATION NUMBER: GB 0126506.5 PRIOR PLICATION NUMBER: GB 0226384.5 PRIOR PLICATION NUMBER: GB 0226384.5 PRIOR PLICATION NUMBER: GB 0203185.4 PRIOR PLILNG DATE: 2001-11-02 PRIOR PLILNG DATE: 2001-11-27 NUMBER OF SEQ 1D NOS: 306 SOFTWARE: Patentin version 3.1 CLENGTH: 3081 TYPE: DNA OVEGANISH: DATE OVEGANISH: DATE OVEGANISH: DATE OVERANISH: DATE: 2002-02-11 OVEGANISH: DATE: 2002-02-11 OVEGANISH: DATE: 2002-02-11 OVEGANISH: DATE: 2002-02-11 OVEGANISH: DATE: 2003-03-11 OVEGANISH: DATE: 2003-03-11 OVEGANISH: DATE: 2003-03-11 OVEGANISH: DATE: 2003-03-11	0 X	AAACTAAAAAATIGIGITGCIGACACCIGGCGCTIGCAAAACTATITCTAGCAGATITI	AAACTAAAAATTGTGTTGCTGACATCTGGTCGCTTGCAAAACTATTTCTAGCAGATTTT	GTGATATITCGTTGGATGGATAAATCCGCCAGTTTTTTTTAATGGAAAGTGCT	GTGATATTTCGTTGTGATCGGTCGATAAATCCGCCAGTTTTTTTT	AACACATTGTAGCGGTTGGGAAGATAGCAGGAAAGAGCCAGCGGGCTGCCGTTTTTCCTT	AACACATTGTAGCGGTTGGGAAGATAGCAGGAAAGAGCCAGCGGGCTGCTTTTTCCTT
mited a vid arch arch arch arch arch arch arch arch	100.0%; 8 100.0%; F	TGTTGCT	TGTTGCT	TGATCGG	TGATCGG	STTGGGA	STIGGGA
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Publication No. US20050227243A1 GENERAL INFORMATION: APPLICANT: Cyclacel Limited APPLICANT: Cyclacel Limited APPLICANT: Cyclacel Limited APPLICANT: Glover, David APPLICANT: Glover, David APPLICANT: Midgley, Carol TITLE OF INVENTION: Cell Cycle Progres TITLE REFERENCE: 10069/2012 CURRENT APPLICATION NUMBER: BCT/GB02/047 PRIOR APPLICATION NUMBER: PCT/GB02/047 PRIOR APPLICATION NUMBER: GB 0126506.5 PRIOR APPLICATION NUMBER: GB 0126506.5 PRIOR PRILON DATE: 2001-11-05 PRIOR PILING DATE: 2001-01-05 PRIOR PILING DATE: 2001-01-05 PRIOR PILING DATE: 2001-01-05 PRIOR PILING DATE: 2001-01-1 PRIOR PILING DATE: 2001-01-05 PRIOR PI	곁	AACTAA	AACTAA	TGATAT	TGATAT	ACACAT	ACACAT
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PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-02-24
PRIOR PELICATION NUMBER: 60/184,831
PRIOR PELICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FRAESEQ for Windows Version 4.
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Best Local Similarity 100.
Matches 3081; Conservative
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                                         CGCTGCGCTATGCGGATCGTGTCAGGAGCTGGTGGTCAAGGATATCGTCGAAGTTTGCC
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                            AGACGTGCATGATAGCCATGATCTCGCCGGGACTTAGCTCCTGCGAGCACACGCTCAACA
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GENERAL INFORMATION:

FUBLICATION NO. US20050208558A1

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLO00728

FILE REFERENCE: CLO00728

FILE REFERENCE: CLO00728

CURRENT APPLICATION NUMBER: 60/157,832

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR PILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12
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181 AGCGGGGGGAAACGAAGGGCAAGGAGCTGGACGCCATACTCACGCTCAATCCGG 840 841 AGCTAATGCAAGTTCTGAACGCACGCCCCGGAGCCCAGAAAACAAGCCCCG 900	GATTGTCAGCAGAAAAAISCIGAATACAAGAAACCAGTCGATTGATTGTCAGCAAAAGCCAGTCGATTGTCAGCAGCAACTACAAAAGCCAGTCGATTGTCAGCAGCAACTACAAAAAACGCAATTGTCAGCAACAAAAAAAA	GTGGTGGCACCACAACGTCGACCACTGGATTACAGCGTCCACGGTACTCG CTACCGGCCAGCAGCACAACGATCGCCTCGGCGGTGCCTAATAACACATTG [TGATGAACCAGGATCCGGCAATCCAACTGGGGGGGGGGG	CAGIGIGGGGCCAAGGACCCCATTAGCCGCAAGGAGGTCAATCGCAAGGAGATCGATC	168 168 174	GAATGGCGACGTCCTCGCCTACGCCAGACGGGATCGGCCAAAACGCACACCATGGGCG GAATGGCGACGCTTCGCCTACGGCCAGACGGGATCGGCCAAAACGCACACCATGGGCG GAATGGCGACGTGCTTCGCCTACGGCCACGCGATCGGCCAAACGCCACACCATGGGCG GTGAGTTTAATGGAAAGGTGCAGGACTGCAAGAACGCCATCACGCCATGGCGCCCAAGG ATGTCTTTGTGAAAGGTGCAGGACTGCAAGAACGGCCATCACGCCATGGCGGCCAAGG ATGTCTTTGTGACCCTGAATATGCCGCGTTACCGCCCATGAATCTAGTCGTCTCGGCCAAGG ATGTCTTTGTGACCCTGAATATGCCGCGTTACCGCGCCATGAATCTAGTCGTCTCTCGGCCAAGGATCTTTGTGACCCTCGGCCCATGAATCTAGTCGACCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCATGGCCCCATGGCCCCATGGCCCCATGGCCCCATGGCCCCATGGCCCCCATGGCCCCATGGCCCTCGGCCCATGGCCCCATGGCCCTCCGGCCCATGGCCCTCGGCCCATGGCCCTCCGGCCCATGGCCCTCCGGCCCATGGCCCTCCGCCCATGGCCCTCCGCCCATGGCCCTCCGCCCATGGCCCTCCGCCCATGGCCCTCCGCCCATGGCCTCCCACCCCATGGCCCATGCCCCATGCCCCATGCCCCATGCCCATCGCCCATGCCCCATCGACCCCATCGCCCATCGCCCATCGCCCATCGCCCATCGCCCATCGCCCATCCCCCCATCCCCCATCCCCCATCCACCCCATCCCCCATCCCCCATCCCCCATCCCCCATCCACCCCATCCCCCATCCACCCCATCCACCCCATCCACCCCATCCACCCCCC

516 ATCTACGACTAACGGAACTCCTCCTGCAAGCAGTGGAAGTTGCTGTCCATCAAGCAGTAC 575	TACAGGTGGACTCAAGAGGAAGGATCATGGACATGATTACGGTGGGGCAGAGCTCAAG 695	Secont Capatro Capat	IMATCCCACACAATCG 935	cagamagccagtcartccamtccactrarcaccartaccartaccactamarcaccartactamarcaccattraccactamarcaccattraccactamarcaccattraccactamarcaccattraccattraccattraccactamarcaccattraccactamarcaccaccaccactamarcaccaccactamarcaccaccaccaccaccaccactamarcaccaccacacaccaccaccaccaccaccaccaccacc	CAGCGTCCACGGTACTCGCAAGCTGCTACCGGCAGCAGCAAGGATCGCCTCGGCG 117		1296 GCNTTGAAGAGGTGGAGGACTGAAGGACAATCGCGAGAACCGACGCCCCCACAGGCC 1355	1416 ACGGCGAAATGATACGCGAATATCAGAGCACGCTGGAATTTGTGCCGCTGCTCGATGGC 1475	6 daggtcaatcgcaaggaggtcgtcatttcggtgccgcccaaggacatgctcatcgtg 159;
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Qy 3001 TGATGGCCGAATATCGCGCCAAGTTGGCCAAGGAGAGATGCTGTCGTGCAGCTTCAATT 3060 Db 3001 TGATGGCCGAATATCGCGCCAAGTTGGCCAAGGAGGAGATGCTGTCGTGCAGCTTCAATT 3060 Qy 3061 CGCCGAATGGCAAGCGTTAGT 3081 Db 3061 CGCCGAATGGCAAGCGTTAGT 3081	RESULT 3 US-11-097-143-1102 ; Sequence 1102, Application US/11097143 ; Fublication No. US20050208558A1 ; GENERAL INFORMATION: ; APPLICANT: Venter, J. Craig ; APPLICANT: et al.	; TITLE OF INVENTION: DEFECTION KIT, SUCH AS NUCLEIC ACID ; TITLE OF INVENTION: ARRAYS, FOR DEFECTING EXPRESSION OF 10,000 OR MORE ; FILLE REFERENCE: CLO00728 ; CURRENT APPLICATION NUMBER: US/11/097,143 ; CURRENT FILING DATE: 2005-04-04 ; PRIOR APPLICATION NUMBER: 60/157,832 ; PRIOR FILING DATE: 1999-10-05	; PRIOR APPLICATION NUMBER: 60/160,191 ; PRIOR PLING DATE: 1999-10-19 ; PRIOR PILING DATE: 1999-10-28 ; PRIOR PILING DATE: 1999-10-28 ; PRIOR PLING DATE: 1999-11-12 ; PRIOR PLICATION NUMBER: 60/164,769 ; PRIOR PLICATION NUMBER: 60/173,383 ; PRIOR RILING DATE: 1999-12-28	PRIOR PRIOR PRIOR PRIOR PRIOR NUMBER	102 DROSOPHILA -1102	Query Match Best Local Similarity 99.6%; Pred. No. 0; Matches 1552; Conservative () Mismatches 7; Indels 0; Gaps 0; Qy 156 AGCAGGGGGTTTTTCTTTTGTTACCGTGCAGAAAAAGAAA 215 Db 1599 AGCCAGGGGTGCCGTTTTTCTTTTGTTACCGTGCAACGAAAAAGAAA 1658		336 TIGGGITCGATTIAGTIGTCAANGCCTIGAATICGGITCGGCGACCTCGGCACCTCGCACACACTCGGTTCGACTTCCGATTICGACTTCCGATTCGATT	Db 1839 TATCGCTCGTCAAGAAACGAAATAAATTTTTCGACCTAAAAAATCTGACTAAAT 1898 Qy 456 TGTGTTTTTTGTTTATGTATTTAGGCACATTTTGCACCACCACCAACGAGTTACTAC 515

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GGTACCGGGATCTACGCCATGGCACCTCGCGATGTCTTCGAGGAGGTATCGCGCCCGGAG 1092
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                                       CGCTTCGACTACGCCTTCAACGACACGTGCGACAATGCCATGGTATACAAATACACAGCC
                                                                    1770 ACGGGATCGGGCAAAACGCACACCATGGGCGGTGAGTTTAATGGAAAGGTGCAGGACTGC
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Sequence 5290, Application US/20050208558A1

Publication No. US20050208558A1

SERBRAL INPORMATION:

APPLICANT: Verter, J. Craig

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: CL000728
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                                   3039 CACGAGCCGCGCAGCAAGGTCGACCTCACCAAGTTCCTGGAGAACCACAAGTTTCGCTTC
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TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REPERENCE: CLOO0728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: 06/157,832
PRIOR APPLICATION NUMBER: 60/167,832
PRIOR PILING DATE: 1999-10-019
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR PELING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR PILING DATE: 12000-01-12
PRIOR PELING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR PILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/194,637
PRIOR PILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/194,637
PRIOR APPLICATION NUMBER: 60/194,637
PRIOR PILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/194,637
PRIOR PILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60/194,637
PRIOR PILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 43008
SEQ ID NO 5231
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Pred. No. 1e-157;
0; Mismatches 379; Indels
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Publication No. US200502085BA1
GENERAL INFORMATION:
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Best Local Similarity 68.1%;
Matches 834; Conservative (
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CORGANISM: DROSOPHILA
US-11-097-143-5291
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Best Local Similarity
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US-11-097-143-5291
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Sequence 5990, Application No. US20050208558A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
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CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT PILING DATE: 2005-04-04

PRIOR PLICATION NUMBER: 60/15/,832

PRIOR FILING DATE: 1999-10-05

PRIOR PELICATION NUMBER: 60/160,191

PRIOR PELICATION NUMBER: 60/160,191

PRIOR PELING DATE: 1999-10-19

PRIOR PILING DATE: 1999-10-19

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR PILING DATE: 1999-11-12

PRIOR PILING DATE: 1999-11-2

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR PILING DATE: 1999-12-28

PRIOR PILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: 60/191,637

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008
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0; Mismatches 379;
                 CURRENT FILING NOMBER: 05/11/09/,143
CURRENT FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR PLING DATE: 1999-10-28
PRIOR PLING DATE: 1999-12-28
PRIOR PLING DATE: 1999-12-28
PRIOR PLING DATE: 1999-12-28
PRIOR PLING DATE: 1999-12-28
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-13
PRIOR PLING DATE: 2000-01-13
PRIOR PLING DATE: 2000-01-13
PRIOR PLING DATE: 2000-01-13
PRIOR PLING DATE: 2000-01-2
PRIOR PLING DATE: 2000-01-2
PRIOR PLING DATE: 2000-01-2
PRIOR PLING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
LENGTH: 4190
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68.1%; Pred. No. 1.5
CURRENT APPLICATION NUMBER: US/11/097,143
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US-11-097-143-5290
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Best Local Similarity
Matches 834; Conserv
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APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REPERRNCE: CLOOD728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR PLLING DATE: 1999-10-19
PRIOR PLLING DATE: 1999-10-19
PRIOR PLLING DATE: 1999-10-19
PRIOR PLLING DATE: 1999-10-19
PRIOR PLLING DATE: 1999-10-12
PRIOR PLLING DATE: 1999-11-12
PRIOR PLLING DATE: 1999-12-28
PRIOR PLLING DATE: 2000-01-12
PRIOR PLLING DATE: 2000-02-24
PRIOR PLLING DATE: 2000-02-24
PRIOR PLLING DATE: 2000-02-24
PRIOR PLLING DATE: 2000-03-23
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 2000-03-23
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PRIOR PLING DATE: 2000-03-3
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                                                                              1417 TGGAAGGATCCGAGATCAATAAATCGCTGCTGGTCCTCAAGGAATGCATTCGCGCTCTGG
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Pred. No. 6.5e-140;
); Mismatches 432;
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Best Local Similarity 64.7%;
Matches 822; Conservative
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US-11-097-143-5989/c
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                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                      DB 10; Length 1970;
                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                   Score 505.8; DB 10;
Pred. No. 4.3e-140;
0; Mismatches 432;
                                                                                                                                                                               Query Match
Best Local Similarity 64.7%;
Matches 822; Conservative
                                                           TYPE: DNA ORGANISM: DROSOPHILA
                                                                                                                    US-11-097-143-5990
SEQ ID NO 5990
LENGTH: 1970
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APPLICANT: Bakowicz, Roman
TITLE OF INVENTION: Novel motor proteins and methods for
TITLE OF INVENTION: Novel motor proteins and methods for
TITLE OF INVENTION: Lheir use
FILE REFERENCE: 1042A
CURRENT PELLING NUMBER: US/09/724,215
PRIOR APPLICATION NUMBER: US/09/724,215
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR PILING DATE: 1999-04-20
PRIOR PILING DATE: 1999-06-18
PRIOR PILING DATE: 1999-06-18
PRIOR PILING DATE: 1999-06-18
PRIOR PILING DATE: 1999-06-18
PRIOR PILING DATE: 1000-06-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PESTEED for Windows Version 4.0
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Pred. No. 7.9e-125;
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10651510; Publication No. US20040096949A1; GENERAL INFORMATION:
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                                                                                                                                                                                                   Length 1421;
                                                                                                                                                                                               Score 454.6; DB 7;
Pred. No. 8.3e-125;
0; Mismatches 434;
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Matches 747; Conservative
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                                  ; TYPE: DNA
; ORGANISM: Human
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Sequence 7, Application US/10651510
Publication No. US200400969491
GENERAL INFORMATION:
APPLICANT: Baraud, Christophe
APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: Novel motor proteins and metl;
TITLE OF INVENTION: Lheir use
FILE REFERENCE: 1042A
CURRENT APPLICATION NUMBER: US/10/651,510
CURRENT APPLICATION NUMBER: US/09/724,215
FRIOR APPLICATION NUMBER: US/09/724,215
FRIOR APPLICATION NUMBER: 09/295,612
FRIOR APPLICATION NUMBER: 09/295,612
FRIOR PILING DATE: 1999-04-20
FRIOR FILING DATE: 1999-06-18
FRIOR FILING DATE: 1999-06-18
FRIOR FILING DATE: 2000-06-15
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GENERAL INFORMATION:

APPLICANT: Beraud, Christophe

APPLICANT: Beraud, Christophe

TITLE OF INVENTION: Novel motor proteins and methods for TITLE OF INVENTION: their use

FILE REFERENCE: 1042A

CURRENT APPLICATION NUMBER: US/10/651,510

CURRENT FILING DATE: 2003-08-28

PRIOR APPLICATION NUMBER: US/09/724,215

PRIOR PILING DATE: 1000-11-28

PRIOR PLILING DATE: 1999-04-20

PRIOR PLILING DATE: 1999-04-20

PRIOR PILING DATE: 1999-06-15

PRIOR PILING DATE: 1999-06-15

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 2172
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Pred. No. 1.1e-124;
0; Mismatches 434;
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Best Local Similarity 62.6%;
Matches 747; Conservative C
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                                                        1509 GCTTCCAAATTATTCTTCGAGCTAAAGG-----GAGAATGCATGGCAAGTTCTCTTTGG
                                                                                                                                  TAGATCTGGCAGGAGAGAGGGGGGGAGCCTTCCAGTGCTGACCGGCAGACCCGCA
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; Publication No. US20040096949A1;
; Publication No. US20040096949A1
; APPLICANT: Beraud, Christophe
; APPLICANT: Sakowicz, Roman
; TITLE OF INVENTION: Novel motor proteins and methods for ittle OF INVENTION: their use
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Pred. No. 2.1e-123;
0; Mismatches 387;
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CURRENT APPLICATION NUMBER: US/10/651,510
CURRENT APPLICATION NUMBER: US/09/724,215
PRIOR APPLICATION NUMBER: US/09/724,215
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-06-18
PRIOR PLING DATE: 1999-06-18
PRIOR FILING DATE: 2000-06-15
NUMBER: OF SEQ ID NOS: 16
SEQ ID NO 3
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Best Local Similarity 64.0%;
Matches 698; Conservative
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                                                                                                                                                                                                                                                                                        Length 2865;
                                                                                                                                                                                                                                                                                Query Match
14.7%; Score 453; DB 6; Length 28
Best Local Similarity 62.5%; Pred. No. 3.8e-124;
Matches 746; Conservative 0; Mismatches 435; Indels
                                                                                                                                                                                                 NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20030165924Al 331025.1
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION WUMBER: 60/195,106
PRIOR FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 276
SOFTWARE: PERL PROGRAM
SEQ ID NO 208
LENGTH: 2865
                                                                                                                                                             ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                              DB 7;
                                                                                                                                                                                                                                                                                                                              Score 449.8; DB 7;
Pred. No. 2.2e-123;
          PRIOR APPLICATION NUMBER: US/09/724,215
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 1090-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-05-18
PRIOR FILING DATE: 1999-06-15
PRIOR PRILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FASTSEQ for Windows Version 4.0
2003-08-28
                                                                                                                                                                                                                                                                                                                          14.6%;
64.0%;
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 64.0
Matches 698; Conservative
                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                       SEQ ID NO 9
LENGTH: 1304
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                              ACGGCCAGACGGGCAAAACGCACACCATGGGCGGTGAGTTTAATGGAAAGGTGC
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        ACAAGTTTCGCTTCGACTACGCCTTCAACGACACGTGCGACAATGCCATGGTATACAAAT
                                                                                  1702 ACACAGCCAAGCCGTTGGTGAAAACCATTTTCGAGGGGGGAATGGCGACGTGCTTCGCCT
                                                                                                                    301 TCACAGCAAGGCCACTGGTACAGACAATCTTTGAAGGTGGAAAAGCAACTTGTTTTGCAT
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Publication No. US20040096949A1
Publication No. US20040096949A1
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: Novel motor proteins and methods for
TITLE OF INVENTION: their use
FILE REPERENCE: 1042A
CURRENT APPLICATION NUMBER: US/10/651,510
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US-10-651-510-9
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0	; TYPE: DNA; Homo sapiens ; ORGANISM: Homo sapiens US-09-954-456-77 Query Match Best Local Similarity 62-4%; Pred. No. 3.4e-123; Matches 744; Conservative 0; Mismatches 437; Indels 12; Gaps 2; Qy 1300 TGAAAGAGGTGGAGGAGAATCGCGAAAGGAAGCGACGCCCGACAGGCCGAGA 1359

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GCAAAACGCACCATGGGCGGTGAGTTTAATGGAAAGGTGCAGGACTGCAAGAACGGCA 1839
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                                          TGAAAACCATTTTCGAGGGGGGAATGGCGACGTGCTTCGCCTACGGCCAGACGGGATCGG 1779
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Job time : 2384 secs
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                                                                                                                                      Sequence 710, Application US/09954456

| Patent No. US2020115057A1
| Patent No. US2020115057A1
| APPLICANT: Young, Paul
| TITLE OF INVENTION: Sets
| TITLE OF INVENTION: Sets
| FILLE REPRENCE: 69229-76
| CURRENT APPLICATION WUMBER: US/60/233,617
| PRIOR PLING DATE: 2000-09-18
| PRIOR PLING DATE: 2000-09-26
| PRIOR PAPLICATION NUMBER: US/60/234,923
| PRIOR PAPLICATION NUMBER: US/60/234,923
| PRIOR PAPLICATION NUMBER: US/60/235,134
| PRIOR PLING DATE: 2000-09-26
| PRIOR PAPLICATION NUMBER: US/60/235,134
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| PRIOR PLING DATE: 2000-09-26
| PRIOR PLING DATE: 2000-09-27
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   1766 CCTGTGAATATACTTTTAAACACCCTGAGATATGCAGACAGGGTCAAGGAGCTG 1818
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3.4e-123;
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Pred. No. 3.4e-
0; Mismatches
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SEQ ID NO 710
LENGTH: 2740
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Best Local Simi:
Matches 744; (
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Sequence 75421, A

Sequence 84, Sequence 19,

Sequence 74421, A Sequence 1607, Ap Sequence 16084, Sequence 160, App Sequence 161, App Sequence 185, App Sequence 13248, A Sequence 13285, A Sequence 13285, A Sequence 13283, A Sequence 13385, A Sequence 16441, A Sequence 171, Appl Sequence 71, Appl Sequence 711, App

Sequence Sequence Sequence

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us-10-840-060-142.rnpbn

Perfect score:

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Sequence:

Scoring table:

Searched:

Database

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Sequence 3433, Application US/11128061
| Publication No. US20060003958A1
| GENERAL INFORMATION:
| APPLICANT: Mounts, William W. APPLICANT: Mounts, William M. APPLICANT: Mounts, Martin S. APPLICANT: Brown, Eugene E. APPLICANT: Brown, Eugene E. APPLICANT: Brown, Eugene E. APPLICANT: Brown, Eugene E. APPLICANT: MOUNTS ECONOMINES W. APPLICANT: MILLIE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
| TITLE OF INVENTION: TO MONITOR GENE EXPRESSION |
| TITLE OF INVENTION: TO MONITOR GENE EXPRESSION |
| TITLE OF INVENTION: TO MONITOR GENE EXPRESSION |
| TITLE OF INVENTION: TO WONER: US/11/128,061 |
| CURRENT APPLICATION NUMBER: US 60/570,425 |
| PRIOR FILING DATE: 2004-05-11 |
| NUMBER OF SEQ ID NOS: 7285 |
| SOFTWARE: PALENTIN VERSION 3.3 |
| LENGTH: 2703 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 461.4; DB 17; Length
Pred. No. 1.1e-107;
0; Mismatches 476; Indels
1 US-10-932-182A-84
1 US-10-932-182A-84
1 US-10-932-182A-75421
1 US-10-932-182A-75421
1 US-10-932-182A-75421
1 US-10-932-182A-75421
1 US-10-932-182A-75421
1 US-10-932-182A-75421
2 US-10-995-561-160
0 US-10-995-561-161
0 US-10-995-561-187
1 US-10-995-561-187
1 US-10-995-561-187
1 US-10-995-561-187
1 US-10-995-561-1828
1 US-10-995-561-1828
1 US-10-995-561-1828
1 US-10-995-561-1828
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US-09-925-065A-119416
US-109-925-065A-508385
US-10-932-182A-82043
US-10-932-182A-82043
US-11-136-527-2116
US-11-136-527-2116
US-11-136-527-2116
US-11-136-527-2116
US-11-136-527-548
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Conservative 0;
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US-11-128-061-3433
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nes 779; Conserv
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US-11-128-061-3433
                                                Query Match
Best Local Si
Matches 779,
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Sequence 137, Appl
Sequence 101, Appl
Sequence 299, Appl
Sequence 7075, Appl
Sequence 762, Appl
Sequence 762, Appl
Sequence 106865;
Sequence 201, Appl
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9260.073 Million cell updates/sec
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| SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq1:*
| SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq1:*
| SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq1:*
| SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
| SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq1:*
| SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
| SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
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| SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
| SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
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| SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
| SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
| SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
| SIDSS/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
| SIDSS/ptodata/2/pubpna/US00_NEW_PUB.seq3:*
| SIDSS/ptodata/2/pubpna/US01_NEW_PUB.seq3:*
                                                                                                                                       May 12, 2006, 21:31:34 ; Search time 1357 Seconds
                   GenCore version 5.1.8
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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VS-11-128-049-3433

VS-11-145-307A-22

US-10-955-054A-101

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US-10-956-054A-101

US-10-960-41-299

VS-11-128-061-7075

VS-11-128-061-7075

US-11-072-512-762

US-10-301-480-106865

US-10-301-480-106865

US-10-301-480-106865

US-11-0301-480-106865

US-11-0301-480-106865

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US-11-0301-480-106865
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                                                                                                                                                                                                                                                                                                                                                                            9312410 seqs, 2039259788 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA_New:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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3081
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Match
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1286 GCGATCGCACGCATTGAAAGAGTGGAGCGACTGAAGGAGAATCGCGAGAAGCGACGCGC 1345

541 GGAGGCAGAAGAGCAAGTCCATCCCACCCGAAGCACATCTTCTGCAAAACCCTGCTCGGAG

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                                                                                                                                                                                                                            TGAAAGAGGTGGAGGACTGAAGGAGAATCGCGAGAAGCGACGCCCCGACAGGCCGAGA
                                                                                                                                                                                                                                                             TGAAGGAAGTGGAAAAATGAAGAACAAGCGAGAAGAAGAAGAAGAAGGCCCAGAACTCTGAAA
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                                                                                                                                                                                                                                                                                                                                       raagaargaagaaga----crcaggagrargacagracrrrccaaacrggaarrrg
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                                                                                                                                                                                         12;
                                                                                                                                                       Length 2832;
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                                                                                                                                                   Score 453; DB 14;
Pred. No. 1.6e-105;
0; Mismatches 435;
 NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
                                                                                                                                                     14.7%;
                                                                                                                                                                                         Conservative
                                                                                                                                                                      Similarity
                                                                           TYPE: DNA
ORGANISM: Homo
                                                                                                              US-11-145-307A-22
                                                                                                                                                                                      746;
                                                          LENGTH: 2832
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Matches 746
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Publication No. US20060094035A1
GENERAL INFORMATION:
APPLICANT: Arcturus Bioscience, Inc.
APPLICANT: Erlander, Mark G.
APPLICANT: Mark Tano-Uni
TILE OF INVENTION: Identification of Tumors
FILE REFERENCE: 022041-002020US
CURRENT APPLICATION NUMBER: US/11/145,307A
CURRENT FILING DATE: 2005-06-03
PRIOR APPLICATION NUMBER: US 60/577,084
PRIOR FILING DATE: 2004-06-04
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| Sequence 10.1 Application WS/10955054A
| Publication No. US20050266420A1
| GENERAL INFORMATION:
| APPLICANT: FUGATH, LAJOS
| APPLICANT: SYMMANS, W. FRASER
| APPLICANT: AYERS, MARK
| APPLICANT: AYERS, MARK
| APPLICANT: AYERS, MALT
| APPLICANT: AYERS, WALT
| APPLICANT: AYERS
| APPL
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Publication No. US20050266420A1
GENERAL INFORMATION:
APPLICANT: BUSZTAL, LAJOS
APPLICANT: BYERS, KENNETH R.
APPLICANT: HESS, KENNETH R.
APPLICANT: AYERS, MARK
APPLICANT: AYERS, MARK
APPLICANT: AYERS, MARK
FILE REFERENCE: UTXC:880US
CURRENT APPLICATION UNMBER: US/10/955,054A
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 137
LENGTH: 2401
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TGAAGGAAGTGGAAAAAATGAAGAACAAGGGAGAAGAAGAAGAAGGAGAAGTCTGAAA
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                                                                                                                       TGGAGGGTGCCGAGATTAACAAATCGCTGCTGGCCCTCAAGGAGTGCATTCGTGCGTTGG
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Best Local Similarity 62.4%; Pred. No. 1e-104;
Matches 744; Conservative 0; Mismatches 437; Indels
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ORGANISM: Homo sapiens
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APPLICANT: MILLER, LANCE D.
APPLICANT: GEORGE, JOSHY
APPLICANT: GEORGE, JOSHY
APPLICANT: GEORGE, JOSHY
APPLICANT: VEGA, VINSENBIUS B.
TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
TITLE OF INVENTION: PROCNOSIS, AND DIAGNOSIS OF CANCERS
FILE REFERENCE: 38271-76067
CURRENT APPLICATION NUMBER: US/10/960,414
CURRENT FILING DATE: 2004-10-06
NUMBER OF SEQ ID NOS: 500
SOFTWARE: PATENTIN VERSION 3.3
                                                                        CGTTCATTGGCGAGAAGAGCAAGACGTGCATGATAGCCATGATCTCGCCGGGACTTAGCT
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14.6%; Score 449.8; DB 13; Length
Best Local Similarity 62.4%; Pred. No. 1e-104;
Matches 744; Conservative 0; Mismatches 437; Indels
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ORGANISM: Homo sapiens
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                                                             Score 449.8; DB 10; Length 2740;
Pred. No. 1e-104;
0; Mismatches 437; Indels 12;
                                                               14.6%;
62.4%;
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    sapiens
                                                                                 Similarity
; ORGANISM: HOMO
US-10-955-054A-101
                                                                                 Best Local Simi
Matches 744;
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          ; ORGANISM: Cricetulus griseus
US-11-128-061-7075
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                                                                                       Best Local Similarity 69.6
Matches 346; Conservative
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APPLICANT: Martalebois, Timochy S.
APPLICANT: Chartalebois, Martin S.
APPLICANT: Binacore, Martin S.
APPLICANT: Brown, Eugene L.
APPLICANT: Miller, Christopher P.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION
FILE REPERBRENCE: 01997.027701
CURRENT APPLICATION NUMBER: US 60/570,425
FRIOR PRICATION NUMBER: US 60/570,425
PRIOR PILING DATE: 2004-05-11
PRIOR PILING DATE: 2004-05-11
SHIOR PILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: Patentin version 3.3
SOFTWARE: Patentin version 3.3
SOFTWARE: LANG
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Publication No. US20060003958A1
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APPLICANT: Melville, Mark W,
APPLICANT: Melville, Mark W,
APPLICANT: Mounts, William M.
APPLICANT: Hounts, William M.
APPLICANT: Hann, Louane E.
APPLICANT: Hann, Louane E.
APPLICANT: Hann, Louane E.
APPLICANT: Brown, Bugene E.
APPLICANT: Brown, Bugene E.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR!
FILE REPERENCE: 01997.027700
CURRENT APPLICATION NUMBER: US/11/128,049
CURRENT APPLICATION NUMBER: US 60/570,425
PRIOR FILING DATE: 2004-05-11
PRIOR FILING DATE: 2004-05-11
NUMBER OF SEQ ID NOS: 7285
SOFTWARE: Patentin version 3.3
SEQ ID NO 7075
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             Length 1400;
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7.9%; Score 21., 69.6%; Pred; No. 9e-52; +ive 0; Mismatches 145; Indels
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SEQ ID NO 762

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                                                     GTAAACAGCAAGTGCAGGTGGTGGACTCACCGAGAAGGTGGTCGATGGCGTCGAGGAGG 2055
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     Pred. No. 9e-52;
); Mismatches 145; Indels
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APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
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SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
Best Local Similarity 69.6%;
Matches 346; Conservative
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NAGAI, KEIICHI
IRIE, RYOTARO
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Publication No. US200
GENERAL INFORMATION:
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US-09-525-065A-5628
; Sequence 562B, Application US/09925065A
; Sequence 562B, Application US/09925065A
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; TITLE OF INVENTION: NUMBER: US/09/925,065A
; CURRENT APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-11-20
; PRIOR PILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR PILING DATE: 2001-01-6
; PRIOR PILING DATE: 2001-01-16
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                                                                                                                                                                                                                                                     Length 3159
                                                                                                                                                                                                                                                                                                                                           0; Mismatches 270; Indels
                                                                                                                                                                                                                                                2.7%; Score 82; DB 18; 49.5%; Pred. No. 1.9e-10;
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                                                                                                                                                                                                                                                                                             Best Local Similarity 49.5
Matches 273; Conservative
; LENGTH: 3159
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-512-762
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Sequence 720244, Application US/10301480
| Publication No. 1920060057564A1
| GENERAL INFORMATION:
| APPLICAMY: Wang, David G. |
| TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms |
| TITLE OF INVENTION: In the Human Genome |
| FILE REFERENCE: 108827.137 |
| CURRENT PILLNG DATE: 2002-11-21 |
| PRIOR PILLNG DATE: 2002-08-09 |
| PRIOR PILLNG DATE: 2002-08-09 |
| PRIOR FILING DATE: 2001-08-10 |
| NUMBER OF SEQ ID NOS: 1226848 |
| SOFTWARE FRANCE FRANCE |
| SOFTWARE FROM SECTION NUMBER: US 60/311,695 |
| PRIOR FILING DATE: 2001-08-10 |
| NUMBER OF SEQ ID NOS: 1226848 |
| SOFTWARE FRANCE FRANCE |
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                    179 CAGCTTCTCACAGCTACGATGAGAGCCTCTCCACCTTGCGCTTTGCCAACCGAGCCAAGA 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2251 AGACGCGTATGGAGGGTGCCGAGATTAACAAATCGCTGCTCGAGGAGGAGTGCATTC
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Pred. No. 4.8e-05;
0; Mismatches 101;
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Publication No. US20060029945A1
GENERAL INCRWATION:
APPLICANT: ISOGAI, TAKAO
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
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YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                                               2488 AGCTGGTGGTCAAG 2501
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                                                                                                                                                                              ACATCAAGAACAAG 252
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IRIE, RYOTARO
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US-11-072-512-201/c
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LENGTH: 730
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Matches 147;
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Publication No. US20060057564A1

Publication No. US20060057564A1

RENERAL INFORMATION:

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: In the Human Genome

TITLE OF INVENTION: In the Human Genome

FILE REFRENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT APPLICATION NUMBER: US 10/215,598

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: PRESEQ FOR Windows Version 4.0

SEQ ID NO 106865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 cadetrericacaderadeareadeacerericacerridecerrideceaaceaaga 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AGAGGCCTAAGGAAGCCTCCCAAAATCAACCTCTCATTATCTGCCCTGGGCAACGTGATTG 61
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Pred. No. 4.8e-05;
0; Mismatches 101; Indels 6
                                                                                                                                                                                                                                                                                              Length 730;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 101;
                                                                                                                                                                                                                                                                                 Query Match 2.0%; Score 60.4; DB 7;
Best Local Similarity 57.9%; Pred. No. 4.8e-05;
Matches 147; Conservative 0; Mismatches 101;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5628
LENGTH: 730
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Best Local Similarity 57.9%;
Matches 147; Conservative
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                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-106865
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                                                                                                                        TYPE: DNA
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2318 GGGCAAACAGTCGGCCCACTTGCCCTTCCGTGTCTCCAAACTCACCCAGGTGCTGCGGGA 2377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 TTCACTA---GGAGGAACTTGTAACACTGATGATTGCAAACATAAGCCCAAGTAACCT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 CTCATTTGGTGAAÁCTCAGAACACAGTTCATTGGGCTGATAGAGCCAAGGAGATTCGGGC 282
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Publication No. US20060046253A1

GENERAL INFORMATION:
APPLICANT: NAKAWURA, VOCHIHIRO
APPLICANT: NAKAWURA, TOKHIHIRO
APPLICANT: NODAWA, YUNIKO
APPLICANT: ASHIKARI, TOKHIHIKO
APPLICANT: ASHIKARI, TOKHIHIKO
TITLE OF INVENTION: NETHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
FILE REFERENCE: 030665-043
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT APPLICATION NUMBER: US/10/932,182A
CURRENT APPLICATION NUMBER: D04-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: PATENTIN version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2258 TATGGAGGTGCCGAGATTAACAAATCGCTGCTGGCCCTCAAGGAGTGCATTCGTGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2438 CTCCTGCGAGCACACGCTCAACACGCTGCGCTATGCGGATCGTGTCAAGGAGCTGGTGGT
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Pred. No. 0.0074;
0; Mismatches 136; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.6; DB 18;
Pred. No. 0.0017;
0; Mismatches 109;
                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1). (1297)
; OTHER INFORMATION: Ceres Seq. ID no. 14304950
US-11-096-568A-4896
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
SEQ ID NO 4896
LENGTH: 1297
TYDE: ...
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Best Local Similarity 53.04
Matches 160; Conservative
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Matches 133; Conservative
                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Glycine max
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US-10-932-182A-84
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Sequence 4896, Application US/11096568A
Sequence 4896, Application No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nickolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCAGGTGACCGTGCGCCAGCCGGGTCAAGAACATCTTGCAGGAGGTGCGGCAG 1238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1120 TGCATCAACGCCCTGAGCGACAAGGGTAGCAACAAGTACATCAACTATCGCGACAGCAAG 1061
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pred. No. 0.0012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 266;
        APPLICANT: SEKI, NACHIKO
APPLICANT: YOSHIKAMA, TSUTOMU
APPLICANT: OTSUKA, MOTOVUKI
APPLICANT: OTSUKA, MOTOVIKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVABL full length cDNA
FILE REFERENCE: 084335-0191
CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
NUMBER OF SEQ ID NOS: 4096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.8%;
Best Local Similarity 49.0%;
Matches 270; Conservative
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17465, A
31072, A
14823, A
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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/cgn2_6/ptodata1/ina/5_COMB.seq:*
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/cgn2_6/ptodata1/ina/H_COMB.seq:*
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/cgn2_6/ptodata1/ina/PP_COMB.seq:*
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US-09-595-684B-24
US-09-620-312D-294
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Sequence 5, Appli
Sequence 1, Appli
US-09-949-016-5573

US-09-620-312D-293

US-09-722-129-1

US-09-722-129-1

US-09-967-908A-7

US-10-159-151-7

US-09-967-908A-9

US-10-159-151-9

US-10-159-151-9

US-10-159-151-5

US-10-159-151-5

US-10-159-151-5

US-10-159-151-5

US-09-967-908A-1

US-09-967-908A-1

US-09-967-908A-1

US-09-967-908A-1

US-09-724-510-1

US-09-724-510-1

US-09-723-216-1

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ALIGNMENTS

CGCAAATGATACGCGAATATCAGAGCACGCTGGAATTTGTGCCGCTGCTCGATGGCCAGG 1479 .540 TCAATCGCAAGGAGATCGATGTCATTTCGGTGCCGCGCAAGGACATGCTCATCGTGCACG 1599 ccccantgarrangaarrrccccracrrrccaarcrcarccacrracrarcacrcarc 1360 TGAAGGAGAAGGTGGCGCTGATGAACCAGGATCCGGCAATCCAAACTGGGAGACGG 82 TGAGAATGAAGAGA-----CTCAGGAGTATGACAGTAGTTTTCCAAACTGGGAATTTG CCGTCGATGACCATCAGATCACAGTGTGCGTGCGCAAGCGTCCCATTAGCCGCAAGGAGG 1300 TGAAAGAGGTGGAGCGACTGAAGGAGAATCGCGAGAAGCGACGCGCCCGACAGGCCGAGA Gaps 12; Length 1292; Indels Score 454.6; DB 3; Pred. No. 6.2e-107; 0; Mismatches 434; Query Match
Best Local Similarity 62.6%;
Matches 747; Conservative (

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TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                  1292
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US-10-112-432-1
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Sequence 1, Application US/10112432
Patent No. 6638754
Patent No. 6638754
Patent No. 6638754
TITLE OF INVENTION: No. 6638754el motor proteins and methods for TITLE OF INVENTION: USE
FILE REFERENCE: 1042A
CURRENT APPLICATION NUMBER: US/10/112,432

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Pred. No. 6.2e-107;
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CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 09/724,215
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-05-18
PRIOR FILING DATE: 1999-05-18
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 1
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62.6%;
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Matches 747; Conservative
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      1540 TCAATCGCAAGGAGATCGATGTCATTTCGGTGCCGCGCAAGGACATGCTCATCGTGCACG
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Patent No. 6638754
GENERAL INFORMATION:
APPLICANT: Berand, Christophe
APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: No. 6638754el motor proteins and methods for
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APPLICANT: Sakwaicz, Roman
TITLE OF INVENTION: No. 6331424el motor proteins and methods for
TITLE OF INVENTION: No. 6331424el motor proteins and methods for
TITLE OF INVENTION: Heir use
FILE REPRENCE: 1042
CURRENT APPLICATION NUMBER: US/09/594,669
CURRENT FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 09/295,612
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: US 09/314,464
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 6.5e-107;
0; Mismatches 434;
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Patent No. 6331424
GENERAL INFORMATION:
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Best Local Similarity 62.6%;
Matches 747; Conservative (
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US-09-594-669-7
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2080 ATGCTGCCCGAACATCCGGCCAGACGTCGGCCAACTCCAATTCGTCGCGTTCGCACGCCG
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; Sequence 13, Application US/09594669
; Patent No. 6331424
; GENERAL INFORMATION:
; APPLICANT: Bacaud, Christophe
; APPLICANT: Bacaud, Christophe
; TITLE OF INVENTION: No. 6331424el motor proteins and methods for IITLE OF INVENTION: their use
; FILE REFERENCE: 1042
CURRENT APPLICATION NUMBER: US/09/594,669
; CURRENT FILING DATE: 2000-06-15
; PRIOR PILING DATE: 1999-04-20
; PRIOR PILING DATE: 1999-04-20
; PRIOR PILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
: LENGTH: 2172
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0; Mismatches 434;
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Matches 747; Conservative
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Pred. No. 6.5e-107;
0; Mismatches 434;
              FILE REFERENCE: 1042A

CURRENT APPLICATION NUMBER: US/10/112,432

CURRENT FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: 09/724,215

PRIOR FILING DATE: 2000-11-28

PRIOR FILING DATE: 1999-04-20

PRIOR PILING DATE: 1999-06-18

PRIOR FILING DATE: 1999-05-18

PRIOR FILING DATE: 1999-05-18

PRIOR FILING DATE: 1999-05-18

PRIOR FILING DATE: 1909-05-18

PRIOR FILING DATE: 1000-06-15

NUMBER OF SEQ ID NOS: 16

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CANT: Beraud, Ch CANT: Sakowicz, OF INVENTION: N	; FILE REPERENCE: their use ; FILE REPERENCE: 1042A ; CURRENT APPLIATION NUMBER: US/10/112,432	PRIOR APPLICATION PRIOR PRIOR FILING DATE: PRIOR FILING DATE: PRIOR APPLICATION N	; PRIOR FILING DATE: 1999-04-20 ; PRIOR APPLICATION NUMBER: 09/314,464 ; PRIOR FILING DATE: 1999-05-18 ; PRIOR APPLICATION NUMBER: 09/594,669	PRIOR FI NUMBER O SOFTWARE SEQ ID NO	; LENGTH: 2172 ; TYPE: DNA ; ORGANISM: Human US-10-112-432-13	Query Match 14.8%; Score 454.6; DB 3; Length 2172; Best Local Similarity 62.6%; Pred. No. 8e-107; Matches 747; Conservative 0; Mismatches 434; Indels 12; Gaps 2	Qy 1300 TGAAAGAGGTGGACTGAAGGAGAATCGCGAGAAGCGACGGCGCGGAGA 135:	Qy 1360 TGAAGGAGGAAGGTGGCGCTGATGAACCAGGATCCGGGCAATCCGAAACTGGGACGG 1419	Qy 1420 CGCAAATGATACGCGAATATCAGAGCACGCTGGAATTTTGTGCCGCTGCTGCATGGCCAGG 1479 Db 692 CCCGAATGATAAAGAATTTTGGGGCTACTTTGGAATGTCATCACTATGACTGATC 751	Qy 1480 CCGTCGATGACCATCAGATCACAGTGTGCGCGAAGCGTCCCATTAGCCGCAAGGAGG 1539 Db 752 CTATCGAAGAGCACAGAATATGTGTTTAGGAAACGCCCACTGAATAAGCAAGAAT 811	Qy 1540 TCAATGGAAGGAGATGGATGATGATCGGGGGAAGGACATGGTCATCGTGCACG 1599 Db 812 TGGCCAAGAAATTGATGTGATTTCCATTCCTAGCAAGTGTCTCCTCTTGGTACATG 871	Qy 1600 AGCCGCGCAGCAAGGTCGACCAAGTTCCTGGAGAACCACAAGTTTCGCTTTCGACT 1659	Qy 1660 ACGCCTTCAACGACACGTGCGACAATGCCATGGTATACAAATACACAGCCAAGCCGTTGG 1719	Qy 1720 TGAAAACCATTTTCGAGGGGGAATGGCGAGGGTTCGCCTACGGCCAGACGGGATGG 1779	Qy 1780 GCAAAACGCACCACCATGGGCGGTGAGTTTAATGGAAAGGTGCAGGACTGCAAGAACGCA 1839 Db 1052 GCAAGACACATACTATAGGGCGGAGACCTCTCTGGGAAAGCCCAGAATGCATCCAAAGGA 1111	Qy 1840 TCTACGCCATGGCGGCCAAGAATGTCTTTGTGACCTGAATATGCCGCGTTACCGCGCA 1899	Qy 1900 TGAATCTAGGCCAGTTTCTTTGAGATTTACAGTGGCAAGGTCTTCGATCTTC 1959 Db 1172 TGGGCCTGGAAGTCTATGTGACATTCTTCGAGATCTACAATGGGAAGCTGTTTGACTGC 1231	Qy 1960 TGTCCGACAAGCAGAAACTGCGCGTCCTGGAGGATGGTAAACAGCAAGTGCAGGTGGTGG
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Patent No. 6331424;
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe;
APPLICANT: Bacwicz, Roman;
TITLE OF INVENTION: No. 6331424e1 motor proteins and methods for;
TITLE OF INVENTION: Their use;
FILE REFERENCE: 1042
CURRENT FILING DATE: 2000-06-15;
PRIOR APPLICATION NUMBER: US 09/295,612;
PRIOR APPLICATION NUMBER: US 09/295,612;
PRIOR APPLICATION NUMBER: US 09/314,464;
PRIOR FILING DATE: 1999-05-18;
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0;
TENDERAL 1312
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Pred. No. 1e-105;
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Sequence 9, Application US/09594669
Sexent No. 6331424
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: No. 6331424el motor proteins and methods for TITLE OF INVENTION: their use
FILE REFERENCE: 1042
CURRENT APPLICATION NUMBER: US/09/594,669
CURRENT PILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 16
NUMBER OF SEQ ID NOS: 16
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Pred. No. 1.1e-105;
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Pred. No. 1e-105;
0; Mismatches 387; Indels
                         TITLE OF INVENTION: No. 6638754el motor prote TITLE OF INVENTION: their use TITLE OF INVENTION: their use TITLE OF INVENTION: their use CURRENT APPLICATION NUMBER: US/10/112,432 CURRENT FILING DATE: 2002-03-29 PRIOR PLING DATE: 2000-11-28 PRIOR PLING DATE: 2000-11-28 PRIOR PLING DATE: 1999-04-20 PRIOR FILING DATE: 1999-04-20 PRIOR FILING DATE: 1999-05-18 PRIOR FILING DATE: 2000-06-15 PRIOR PRIOR PRIOR PRIOR SPECIATION NUMBER: 09/594,669 PRIOR PRIOR PRIOR DATE: 2000-06-15 SOFTWARE: 2000-06-15 SOFTWARE: PRIOR PRI
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Best Local Similarity 64.01
Matches 698; Conservative
    Sakowicz, Roman
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US-10-112-432-3
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Pred. No. 1.1e-105;
0; Mismatches 387;
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 09/724,215
PRIOR FILING DATE: 2000-11-28
PRIOR PILING DATE: 1999-04-20
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 1999-04-20
PRIOR FILING DATE: 1999-05-18
PRIOR FILING DATE: 1999-05-18
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Patent No. 6638754
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Sakowicz, Roman
TITLE OF INVENTION: No. 6638754el motor prot
FILE REFERENCE: 1042A
CURRENT APPLICATION NUMBER: US/10/112,432
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                                     1660 ACGCCTTCAACGACACGTGCGACAATGCCATGGTATACAAATACACAGCCAAGCCGTTGG
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US-09-595-684B-32
Sequence 12, Application US/09595684B
Patent No. 6544766
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Obashi, Cara
APPLICANT: Sakowicz, Roman
APPLICANT: Wood, Kenneth
APPLICANT: Wood, Kenneth
APPLICANT: Yu, Ming
TITLE OF INVENTION: Human kinesins and methods of producing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/09594669
| Patent No. 6331424
| GENERAL INFORMATION:
| APPLICANT: Beraud. Christophe
| APPLICANT: Sakowicz, Roman. TITLE OF INVENTION: No. 6331424el motor proteins and methods for TITLE OF INVENTION: their use
| FILE REFERENCE: 1042
| FILE REFERENCE: 1042
| FILE REFERENCE: 1099-04-10
| FILE REPERENCE: 1999-04-20
| PRIOR APPLICATION NUMBER: US 09/295,612
| PRIOR APPLICATION NUMBER: US 09/314,464
| PRIOR FILING DATE: 1999-04-20
| PRIOR FILING DATE: 1999-04-10
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ilarity 62.4%; Pred. No. 1.5e-105;
Conservative 0; Mismatches 437;
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Best Local Similarity
Matches 744; Conser
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US-09-594-669-15
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                                                                                                                                    1646 GACAGAACAAGGCTCACACCCCGTTCCGTGAGAGCAAGCTGACAGGTGCTGAGGGACT
                                  TTTTCCAGATTGTGCTGCGGCCGCAGGCTCGACGAAGATCCATGGCAAGTTCTCGTTCA
                                                                    1472 GCTTCCAAATTATTCTTCGAGCTAAAGG-----GAGAATGCATGGCAAGTTCTCTTTGG
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APPLICANT: Bakowicz, Roman
TITLE OF INVENTION: No. 6638754e1 motor proteins and meth)
TITLE OF INVENTION: No. 6638754e1 motor proteins and meth)
TITLE OF INVENTION: No. 6638754e1
TITLE OF INVENTION: Libeir use
FILE REPERENCE: 1042A
CURRENT PELING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: 09/724,215
PRIOR APPLICATION NUMBER: 09/724,215
PRIOR APPLICATION NUMBER: 09/3295,612
PRIOR PILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LIENGHAL 2740
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Pred. No. 1.5e-105;
0; Mismatches 437;
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; Patent No. 6638754
; GENERAL INFORMATION:
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Matches 744; Conservative C
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US-10-112-432-15
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TITLE OF INVENTION: and purifying human kinesins FILE REFERENCE: cytop036
CURRENT APPLICATION NUMBER: US/09/595,684B
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 2740
                                                                                                                                                                                                                                                                             14.6%; Score 449.8; DB 3; 62.4%; Pred. No. 1.5e-105; live 0; Mismatches 437;
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Matches 744; Conservative
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Sequence 5, Application US/09849602 Patent No. 6794501 GENERAL INFORMATION: APPLICANT: Scanlan, Matthew J. APPLICANT: Old, Lloyd J.

RESULT 14 US-09-849-602-5

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Pred. No. 1.5e-105;
0; Mismatches 437;
APPLICANT: Stockert, Elisabeth
HAPLICANT: Chen, Yao-Tseng
TITLE OF INVENTION: Colon Cancer Antigen Panel
FILE REFERENCE: L0461/7105 (JRV)
CURRENT APPLICATION NUMBER: US/09/849,602
CURRENT FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
SEQ ID NO 5
LENGTH: 2740
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Fatent No. 6331424
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Barwicz, Roman
TITLE OF INVENTION: No. 6331424e1 motor proteins and methods for
TITLE OF INVENTION: Lheir use
FILE REFERENCE: 1042
CURRENT APPLICATION NUMBER: US/09/594,669
CURRENT FILING DATE: 1999-04-20
FRIOR APPLICATION NUMBER: US 09/295,612
FRIOR APPLICATION NUMBER: US 09/314,464
                                                                                                                                                                                                                                                                                                                                                                                                                                              2440 CCTGCGAGCACACGCTCAACACGCTGCGCTATGCGGATCGTGTCAAGGAGCTG 2492
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65.2%; Pred. No. 1.7e-99;
cive 0; Mismatches 339;
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Matches 645; Conservative
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ORGANISM: Human
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Direct Submission

AL SUBMILLER (102-UTN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRV cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gooegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by patfalal EcokI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and RSY libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

Location/Qualifiers
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A1546445 LD48021.5
B1372858 RE60047.5
B1572859 AT086077.5
AA949737 LD29734.5
B1534473 GM26945.5
B7452432 AT29153.5
B7492432 AT29173.5
B7492432 AT29173.5
B7492432 AT29173.5
A1532286 AT08703.5
A1532286 AT08703.5
A1532286 AT08703.5
A1532286 AT08703.5
B1609578 RH14717.5
B1609578 RH14181.5
A1533352 SD05134.5
B1609400 RH14181.5
A1533352 SD05134.5
B1609400 AT28556.5
B1609731 RH14552.5
B1609731 RH14552.5
B1609731 RH14552.5
B1609731 RH14552.5
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebhydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACROGGO1"
/clone lib="RPCT-98"
/note="end : TET3"
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                                                                                    BI354473
AA952135
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CK660542
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BE975372
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
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KEYWORDS
SOURCE
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LOCUS
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BF499568 AT14153.5
BF48648 AT20744.5
BF498461 AT12870.5
BF489668 AT25778.5
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AT29741.5
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AT13721.5
SD16989.5
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AT30655.5
                                                                                                                                            May 12, 2006, 17:35:46; Search time 11790 Seconds (without alignments) 12226.548 Million cell updates/sec
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LP02741.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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BI609735
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                  GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                             41078325 segs, 23393541228 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       nucleic search, using sw model
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3081
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seq length: 200000000
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9b_est2:.*
9b_htc::.*
9b_est4:.*
9b_est5:.*
9b_est7:.*
9b_gss2:.*
9b_gss2:.*
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                                         Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST:*
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751.6 752.6 750.2 720.2 710.4 710.8 692.8 693.6 674.4 663.8 663.8 663.8

659 656 641 629 625.2 619.6

917

Score

Result . 8

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BF499568
AT1413.5prime AT Drosophila melanogaster adult testes poTB7
Drosophila melanogaster EDNA clone AT14153 5 similar to CG1453:
FBan0001453 'motor protein' located on: X 10A6-10A7;: 04/09/2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev marge="0-3 day old Ore-R males"
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.319: DH5-alpha TonA"
AT.121-AT.319: DH5-alpha TonA"
/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
/note="Organ: ADULT testes, Vector: pOTB7, Site 1: BCoR1,
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid CDNA library."
                                                                                                                                                                                                                                                                                                                   1 (Dases 1 to 779)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E.,
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E.,
Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V.,
Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N.,
Bacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C.,
Lewis, S.E., Celniker, S. and Rubin, G.M.
BDGP/HHMI AT Drosophila EST Project
On Dec 6, 2000 this sequence version replaced gi:11582869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCACAAGTTTATCGCTCGTCAAGAACAACGAAATAAAATTATTTTCGACCTAAAAATC
                                                                                                                                                                                                                                   Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Mustazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE00348: arm:X [10878159,11180508]
estimated-cyto:1083-10181: 04/09/2001
Plate: AT.141 row: E column: 5
High quality sequence stop: 689.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="AT14153"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.7%; Score 761.6; DB 2;
llarity 99.4%; Pred. No. 1.1e-186;
Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
   TYCMCCCATTWAAAAGGTGARCSACTGAAGAAA 1054
                                                                                                                                                                                                       BF499568.2 GI:13691428
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                                                                                                                                                                      mRNA sequence.
BF499568
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                                                                                                                                                   ACAAGTTTATCGCTCGTCAAGAAACAACGAAATAAAATTATTTTCGACCTAAAAATCTG
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                                    Gaps
                                    3,
 Length 1101;
                                  Indels
Score 917; DB 10;
Pred. No. 4e-227;
1; Mismatches 52;
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                                  41;
 29.8%;
                                  Conservative
                   Similarity
                 Best Local Sim:
Matches 957;
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/dev state="0-3 day old Ore-R males"
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="lab" DH5-alpha Tonna"
/clone_lib="AT.319: DH5-alpha Tonna"
/note="Organ: ADULT testes; Vector: pOTB7; Site_1: EccR1;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 752.6; DB 2; Length 759;
Pred. No. 2.4e-184;
0; Mismatches 4; Indels 0;
hit genomic AE003485: arm:X [10878159,11180508]
estimated-cytc:10A3-10B11: 04/09/2001
Plate: AT.207 row: D column: 8
High quality sequence stop: 734.
Location/Qualifiers
                                                                                                                                melanogaster"
                                                                                                                           organism="Drosophila |
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="AT20744"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.4%;
99.5%;
                                                                                                                                                                                                                    /sex="male"
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Drosophila melanogaster
Drosophila melanogaster
Drosophila melanogaster
Sudaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophildee; Drosophila.
Ephydroidea; Lor 759)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E.,
Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V.,
Berman, B., Carlson, J., George, R., Gonzalez, M., Guarin, H., Harris, N.,
Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J.,
Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C.,
Lewis, S.E., Celniker, S. and Rubin, G.M.
BUGF/HHMI AT Drosophila EST Project
Lunpublished (2000)
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AT20744.Sprime AT Drosophila melanogaeter adult testes pOTB7
Drosophila melanogaeter cDNA clone AT20744 5 similar to CG1453:
FBan0001453 'motor protein' located on: X 10A6-10A7;: 04/09/2001,
                                       CAGTCGGGCAAGTGCATCACAGTCGAATGGTACGAGCGGCGGCGAAACGAAGGAGGAG
                                                                                                     ATAGAGATATACAGGTGGAGTCAAAGAGGAAGGATCATGGACATGATTACGGTGGGGCAG
                                                                                                                              ATAGAGATATACAGGTGGAGTCAAAGAGGAAGGATCATGGACATGATTACGGTGGGGCAG
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                                                                                                                                                                                                                    AGCGTCAAGATCAAGCGGACGGATGGCCGGTCCACATGGCCGTGGTGGTGGTCATAAC
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                   AAGCAGTACTCGGAGTTAACGCAGGATAAGCCGGGAGAAAGAGAAAAAAGAGATCGGTGGAGA
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000 this sequence version replaced gi:11569749
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BF486448
BF486448.2 GI:13698328
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Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

Ephydroidea; Drosophilae; Drosophila.

Estableton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, B.,

Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V.,

Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N.,

Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J.,

Pacleb, J., Parsgas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C.,

Lewis, S.E., Celliker, S. and Rubin, G.M.

BDGP/HHMI Ar Drosophila EST Project

Unpublished (2000)
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AT25778.5prime AT Drosophila melanogaster adult testes porTB7
Drosophila melanogaster EDNA clone AT25778 5 similar to CG1453:
FBan0001453 'motor protein' located on: X 10A6-10A7;: 04/09/2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              661 CGTGCTTCGCCTACGGCCAGACGGGATCGGGCAAAACGCACCATGGGCCGGTGAGTTTA 720
                                      CAGCCAGTGCTGGTCCGGCGGCACAGGAGTCGCCACTGCGGGCCACAACCCAGGGAGCTG
                                                                                                       GCGCCCTAGTACCCGGCGATCGCACGCATTGAAAGAGGTGGAGCGACTGAAGGAGAATC
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Drosophila melanogaster

Drosophila melanogaster

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Bndopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophildee; Drosophila.

E (Asses 1 to 763)

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E.,

Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V.,

Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N.,

Li, P., Lido, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J.,

Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C.,

Elewis, S.E., Cellniker, S. and Rubin, G.M.

Bugg/HHMI AT Drosophila EST Project

Unpublished (2000)
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/lab host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab host="Plates AT.10-AT.120: DH5-alpha. Plates
/r.121-AT.319: DH5-alpha TonA"
/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
/note="Organ: ADULT testes; Vector: pOTB7; Site_1: ECORI;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library."
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CGGCCGGCGGAGGTGGTGGCACCACAACGTCGACGACCACTGGATTACAGCGTCCACGGT 720
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763 bp mRNA linear EST 19-APR-200

T12870.5prime AT Drosophila melanogaater adult testes pOTB7

Drosophila melanogaater cDNA clone AT12870 5 similar to CG12192:

FBan0012192 'motor protein' located on: 2R 59D1-59D1;: 04/09/2001,
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: $10 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003485: arm:X [10878159,11180508]
estimated-cyto:10A3-10B11: 04/09/2001
Plate: AT.128 row: F column: 10
High quality sequence stop: 673.
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Contact: Stapleton, M.
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Pred. No. 1e-183;
0; Mismatches 8; Indels
                                                 ACTOGORAGOTGOTACOGGOCAGORGGACAAGGATCG 1167
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|mol_type="mRNA"
|db_xref="taxon:7227"
|clone="AT12870"
                                                                                  ACTCGCAAGCTGCTACCGGCCAGCAGCAGCATCG
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llarity 99.0%;
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1585 TGCTCATCGTGCACGAGCCGCGCAGCAAGGTCGACCTCACCAAGTTCCTGGAGAACCACA 1644
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Email: stephenr@bcm.tmc.edu
NCBI Trace Archive: 226720539
Insert Length: 1750 Std Error: 0.25.
Location/Qualifiers
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/db_xref="taxon:7237"
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/lab host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab host="Plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.131: DH5-alpha TonA"
/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
/note="Organ: ADULT testes; Vector: pOTB7; Site_1: ECORI;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTAATGCAAGATACTGTCGAACAGCACGCCCCCGGAGCCCAAGAAACAAGCCCACCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
               Fax: 510 486 6798
Email: http://www.fruitfly.org/BST, est@fruitfly.berkeley.edu
htt genomic AE003485; arm.X [10878159,11180508]
estimated-cyto:10A3-10B11: 04/09/2001
Plate: AT.257 row. G column: 6
High quality sequence stop: 720.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                          23.4%; Score 720.4; DB 2; Length 722; 99.9%; Pred. No. 5.9e-176; ive 0; Mismatches 1; Indels 0
                                                                                                                            1. .722
/organism="Drosophila melanogaster"
/mol type="mRNA"
/db xref="taxon:7227"
/clone="AT25778"
One Cyclotron Rd, Berkeley, CA 94720, USA
                                                                                                                                                                                                             'sex="male"
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Best Local Simil
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Drosophila pseudoobscura

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 1105)

Richardes, S., Liu, Y., Bettencourt, B.R., Hradecky, P., Letovsky, S.,

Richardes, S., Liu, Y., Mubisz, M.J., Chen, R., Meisel, R.P.,

Couronne, O., Hua, S., Smith, M.A., Zahang, P., Liu, J., Bussemaker, H.J.,

Nalesen, R., Thornton, K., Howells, S.L., Scherer, S.E., Sodergren, E.,

Matthews, B.B., Crosby, M.A., Schorer, S.E., Sodergren, E.,

Rives, C.M., Metzker, M.L., Muzny, D.M., Scott, G., Steffen, D.,

Rives, C.M., Metzker, M.L., Muzny, D.W., Scott, G., Steffen, D.,

Rives, C.M., Metzker, M.L., Muzny, D.W., Scott, G., Steffen, D.,

Rives, C.M., Worley, K.C., Havlak, P., Durbin, K.J., Egan, A.,

Gall, R., Hune, J., Morgan, M.B., Miner, G., Hamilton, C., Huang, Y.,

Waldron, L., Verduzco, D., Clark, P., Clark, A.G., Schaeffer, S.W.,

Gelbart, W., Weinstock, G.M. and Gibbs, R.A.

Comparative genome sequencing of Drosophila pseudoobscura:

chromosomal, gene, and cis-element evolution 1142 1105 bp mRNA linear EST 15-JUN-2005 49335266 Drosophila pseudoobscura embryonic cDNA library Drosophila pseudoobscura cDNA clone G9 5', mRNA sequence. ñ GCTCGATGGCCAGGCCGTCGATGACCATCAGATCACAG-TGTGCGTGCGCAAGCGTCCCA 1524 1525 TTAGCCGCAAGGAGGTCAATCGCAAGGAGATCGATGTCATTTCGGTGCCGCGCAAGGACA 1584 661 GGTGGCACCACAACGTCGACGACCACTGGATTACAGCGTCCACGGTACTCGCAAGCTGCT 720 62 CAAGCCGAAAGGAGGTGAATCCCTAAGAGGTCGATGTCATATCGGTGCCCCGCAAGGACT 121 /note="Vector: pOTB7; Site 1: EcoR1; Site 2: XhoI; oligo dt priming from poly $A \leftarrow RNA$, directionall \overline{y} cloned" deacdaddectendecerrandecearcacearcacearcacecerrandecerandecerene 61 GGTGGCACCACAACGTCGACCACTGGATTACAGCGTCCACGGTACTCGCAAGCTGCT Gaps /dev_stage="0-18h embryos" /clone_lib="Drosophila pseudoobscura embryonic cDNA m m Query Match 23.3%; Score 718; DB 8; Length 1105; Best Local Similarity 83.0%; Pred. No. 2.8e-175; Matches 853; Conservative 0; Mismatches 172; Indels /organism="Drosophila pseudoobscura" Human Genome Sequencing Center Baylor Collage of Medicine One Baylor Plaza, Houston, TX 77030, USA Tel: 713-798-6667

1 Drosophila j Bukaryota; j Neoptera; E Ephydroidea Ephydroidea Richards, S. Nielsen, R., Couronne, O. Wathews, B.! Rives, C.M., Wheeler, D.A Gill, R., Hu Waldron, L., Noor, M.A., Comparative Comparative	년 D H B B B B B B B B B B B B B B B B B B	/or /mo/mo/mo/mo/mo/mo/mo/mo/mo/mo/mo/mo/mo/	Query Match 22.5%; Score 692; DB 8; Length 1153; Best Local Similarity 82.9%; Pred. No. 1.7e-168; Indels 2; Gaps 2; Matches 813; Conservative 0; Mismatches 166; Indels 2; Gaps 2; 1452 GAATTTGTGCCGCTGCTCGATGGCCGCGCTGCATCACCACACACA	GGGCAAGCGTCCACCAAGGAGGAGGAGTCCTTTAGAGGTCGATGTCATATGGT GCGCGCAAGGACATGCTGTGCACGGAGGCGGCAGCAAGGTCGACTCACCAGGT GCGCGCGAAGGACATGCTCATGGAGCGGGGCAGCAAGGTCGACCAAGTT GCCCGCAAGGACTTGATGATGTCCATGAGCGGGGACCAAGGTCGATCTCACCAAGTT CCTGGAGAACCACAAGTTTGGCTTCGACTACGCCTTCAAGGACGAAGATT CCTGGAGAACCACAAGTTTCGCTTTCGACTACGCCTTCAACGACACACGACCAAGATT	199 CCTTGAACATCACAAATTTCGACTATGCTTTCAACGAATGTGTGACAATGCCAT 258 1691 GGTATACAAATACACAGCCAAGCCGATGGTGAAAACGATTTCGAGGGCGGAATGCCAT 258 1692 GGTGTACAAATACACAGCCAAGCCGTTGGTGAAAACTATTTTCGAGGGCGGAATGGCGAC 1750 1751 GTGCTTCGCCTACGGCCAAGCCCTGGTGAAAACTATTTTCGAGGGCGGAATGGCGAC 318 1751 GTGCTTTGCCTACGGCCAGAGGATCGGGCAAAAACGCACCATGGCGGGGAGTTTAA 1810 1151 TGGAAAGGTGCCAGACAGAACGCAACCATGGCGGGGGAGTTTAC 378 1811 TGGAAAGGTGCAGGACTGCAAGAACGGCATCACCATGGCGGGGGAGTTTAC 378 1811 TGGAAAGGTGCAGGACTGCAAGAACGGCATCTACGCCATGGCGGGGAGGTTTTGT 1870 179 GGGTAAAATACAGGACTGCAAGAACGCATCTATGCCCATGGCCGCCAAGGATGTTTGC 438
ORGANISh REFERENCE AUTHORS TITLE	JOURNA PUBME COMMENT COMMENT FEATURES	ORIGIN	Que Bes Mat Qy Db	8 8 8 8	8 6 8 6 8 6 8
	Db 362 ACTGCAAGAACGGCATCTATGCCATGGCCCAAGATGTGTTCGCGACCCTCAATACAC 421	TCATCCAGCACGGCAATGCTGCCCGAACATCCGGCCAGACGTCGGCCAACTCCAATTCGT	Db 722 GTAAATTTTGGTTGGTGGGGGGGGGGGGGGGGGGGGG	2365 AGGTGCTGC	Oy 2485 AGGAGTG 2492 Db 1020 AGGAACTG 1027 RESULT 7 BR135726 LOCUS DEFINITION 49291254 Drosophila pseudoobscura embryonic cDNA library Drosophila pseudoobscura cDNA clone 13 5', mRNA sequence. ACCESSION DR135726 VERMORDS VERMORDS SOURCE SOURCE SOURCE SOURCE DESCRIPTION 49291254 Drosophila pseudoobscura cDNA concentration of the co

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/dev gragge="0-3 day old Ore-R males"
/lab host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab host="Plates AT.10-AT.120: DH5-alpha. Plates
/r.121-AT.319: DH5-alpha TonA"
/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
/note="Organ: ADULT testes; Vector: pOTB7; Site_1: BCoRI;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library."
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                                                                            1. .720
/organism="Drosophila melanogaster"
/mol_type="mRNA"
/db_xref="taxon:7227"
/clone="A713454"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                    Score 685.8; DB 2;
Pred. No. 6e-167;
); Mismatches 8;
           estimated-cyto:10A3-10B11: 04/09/2001
                         Plate: AT.134 row: E column: 6
High quality sequence stop: 660.
Location/Qualifiers
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AT13454.5prime AT Drosophila melanogaster adult testes pOTB7
Drosophila melanogaster cDNA clone AT13454 5 similar to CG1453:
FBan0001453 'motor protein' located on: X 10A6-10A7;: 04/09/2001,
                                                                                                           558
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopteryota; Diptera; Bachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila;
1 (bases 1 to 720)
2 (Sapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E.,
Berman, B., Carlson, J., Champe, M., Chawyez, C., Chew, M., Dorsett, V.,
Parfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N.,
Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C.,
Lewis, S.E., Celniker, S. and Rubin, G.M.
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                                                                                                                                                                 GACCCTGAATATGCCGCGTTACCGCGCGATGAATCTAGTCGTCTCGGCCAGTTTCTTTGA
                      GATTTACAGTGGCAAGGTCTTCGATCTTCTGTCCGACAAGCAGAAACTGCGCGTCCTGGA
                                                                                         GGATGGTAAACAGCAAGTGCAGGTGGTGGACTCACCGAGAAGGTGGTCGATGGCGTCGA
                                                                                                                                                                                                               GGAGGTACTGAAGCTCATCCAGCACGGCAATGCTGCCCGAACATCCGGCCAGACGTCGGC
                                                                                                                                                                                                                                    CAACTCCAATTCGTCGCGTTCGCACGCCGTTTCCAGATTGTGCTGCGGCCGCAGGGCTC
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ONE CYCLOLYON RG, BERKELEY, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003485: arm:X [10878159,11180508]
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On Dec 6, 2000 this sequence version
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BF498964
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Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Boptorera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

Estapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E.,

Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V.,

Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N.,

Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J.,

Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C.,

Lewis, S.E., Celniker, S. and Rubin, G.M.

BDGP/HHMI AT Drosophila EST Project

Ly Unpublished (2000)
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121 CGGAACTCCTCCTGCAAGCAGTGGAAGTTGCTGTCCATCAAGCAGTACACGGAGTTAACG 180
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AT04507.5prime AT Drosophila melanogaster adult testes pOTB7
Drosophila melanogaster cDNA clone AT04507 5 similar to CG1453:
FBBAN0001453 'motor protein' located on: X 10A6-10A7;: 04/07/2001,
                                                                                                                                                                                                                               541 AATCTCACCAGCCGTATGACCATGGCCGGAAACATGCTGAACAAAATCCAGGAAAGGCCAG
                                                             CAGGATAAGCCGGGAGAAAGAGAAAGAGATCGGTGGAGAATAGAGATATACAGGTGGAGT
                                                                                                                                                                                            CAAAGAGGAAGGATCATGGACATGATTACGGTGGGCCAGAGCGTCAAGATCAAGCGGACG
                                                                                                      181 CAGGATAAGCCGGGAGAAAGAAAAGAAATCGGTGGAGAATAGAGATAATAGAGATAATAGAGTGGAGT
                                                                                                                                                                                                                                                                                                                           GATGGCCGCCCCCCCCCCTGGTGGCGGTGATCAACCAGTCGGGCAAGTGCATCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCGAATGGTACGAGCGCGGCGAAACGAAGGCCAAGGAGGTAGAACTGGACGCCATACTC
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003485: arm:X [10878159,11180508]
estimated-cyto:1083-10811: 04/07/2001
Plate: AT.45 row: A column: 7
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Contact: Stapleton, M.
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/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.33: DH5-alpha TonA.
folone_lib="AT Drosophila melanogaster adult testes pOTB7"
/note="Organ: ADULT testes; Vector: pOTB7; Site_1: ECORI; Site_2: Xhol; The mRNA for the testis library was made from testes and seminal vessicles hand dissected from 0-3 day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into pOTB7. Plasmid cDNA library."
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Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V.,
Barfan, D., Frise, E., George, R., Gonzalez, M., Guartin, H., Harris, N.,
Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J.,
Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C.,
BDGP/HMI AT Drosophila EST Project
Unpublished (2000)
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702 bp mRNA linear EST 23-APR-20 AZ9741. Sprime AT Drosophila melanogaster adult testes pOTB7 Drosophila melanogaster cDNA clone AT29741 5 similar to CG1453: FBan0001453 'motor protein' located on: X 10A6-10A7;: 04/09/2001,
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 466 6798
Fig. 510 466 6798
Fig. 510 466 6798
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Fig. 680.
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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|mol_type="mRNA"
|db_xref="taxon.7227"
|clone="AT29741"
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llarity 99.3%; Pred. No. 2.2e-166;
Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
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BG633810.1 GI:13761347
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BG633810
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SM Drosophila melandogaeter (Intil Lify)
Drosophila melandogaeter
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Medoterygota; Diptera; Brachycera; Muscomorpha;
Rooptera; Endoterygota; Drosophilidae; Drosophila.

Ephydroidea; Drosophilidae; Drosophila.

Stapleton, M. Brokerein, P., Hong, L., Agbayani, A., Baxter, E.,
Earlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V.,
Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N.,
Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J.,
Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C.,
Lewis, S.E., Celniker, S. and Rubin, G. M.
BDGF/HMI AT Drosophila EST Project
Unpublished (2000)
On Dec 6, 2000 this sequence version replaced gi:11582505.
                                                 BE499204
AT13721.Sprime AT Drosophila melanogaster adult testes pOTB7
Drosophila melanogaster CDNA clone AT13721 5 similar to CG1453:
FBan0001453 'motor protein' located on: X 10A6-10A7:: 04/09/2001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /notes Torgan: ADULT testes; Vector: pOTP7; Site 1: BCORI; Site 2: Xhol; The mRNA for the testis library was made from testes and seminal vessicles hand dissected from 0-3 day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated CDNAs were directly ligated into pOTB7. Plasmid CDNA library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Pax: 510 486 6498
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003485: arm:X [10878159,11180508]
hit genomic AE001485: arm:X [10878159,11180508]
estimated-cyc.10A3-10B11: 04/09/2001
Plate: AT.137 row: B column: 9
High quality sequence stop: 609.
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/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.319: DH5-alpha TonA"
/clone_lib="AT Drosophila melanogaster adult testes
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Pred. No. 6.4e-165;
0; Mismatches 5;
                                                                                                                                                                                                                       Drosophila melanogaster (fruit fly)
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="AT13721"
                                                                                                                                                    BF499204
BF499204.2 GI:13691069
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Best Local Similarity 99.3%;
Matches 681; Conservative
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                                                                                                                                      mRNA sequence.
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DEFINITION
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
COMMENT
      RESULT 11
BF499204
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AT.121-AT.1319: DH5-alpha TonA.
AT.121-AT.1319: DH5-alpha TonA.
/clone lib="AT Drosophila melanogaster adult testes pOTB7"
/clone lib="AT Drosophila melanogaster adult testes pOTB7"
/note="Organ: ADULT testes; Vector: pOTB7; Site 1: ECORI;
Site 2: Xho1; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library."
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                                                              organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 680.6; DB 2;
Pred. No. 1.3e-165;
                                                                                                                                                                                                                                                                                                                                                                                                                   22.1%; Sco. . .... 99.4%; Pred. No. 1...
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High quality sequence stop: 643.
Location/Qualifiers
                                                                                /mol_type="mRNA"
/db_xref="taxon:7227"
/clone="AT04507"
                                                                                                                                                    sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             683; Conservative
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/note="Vector: pOT2; Site 1: BcoRI; Site 2: Xho1; Sized fractionated cDNAs were directly ligated into pOT2. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                   66 TCTGACTAAATTGTGTTTTTTGTTTTATGTATTTTAGGCACATTTTGCACACCCACACA
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                     Length
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                                                                                                   Score 674.4; DB 3;
Pred. No. 5.6e-164;
                                                                                                                                          0; Mismatches
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BF495237.2 GI:13685720
                                                                                                 21.9%;
                                                                                                                      Best Local Similarity 99.1
Matches 678; Conservative
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BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                           TAGAGATATACAGGTGGAGTCAAAGAGGAAGGATCATGGACATGATTACGGTGGGGCAGA
                                                                                                                      AGTCGGGCAAGTGCATCACAGTCGAATGGTACGAGCGCGGCGAAACGAAGGCCAAGGAGG
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                    TAGAGATATACAGGTGGAGTCAAAGAGGAAGGATCATGGACATGATTACGGTGGGGCAGA
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                                                                                                 GCGTCAAGATCAAGCGGACGGATGGCCGCGTCCACATGGCCGTGGTGGCGGTGATCAACC
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One Cyclorron Rd, Berkeley, CA 94720, USA
Fax: 510 486 Serveley, CA 94720, USA
Fax: 510 486 Serveley, CA 94720, USA
Fax: 510 486 Serveley.
Hit genomic AE003485: arm:X [10878159,11180508]
estimated-cyto:10A3-10B11: 05/18/2001
estimated-cyto:10A3-10B11: 05/18/2001
Flate: SD.169 row: H column: 5
High quality sequence stop: 679.
Location/Qualifiers
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:71227"
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Drosophila melanogaster (fruit fly)

Brosophila melanogaster

Bukaryora; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bukaryora; Bardopterygota; Diptera; Brachycera; Muscomorpha;

Bphydroidea; Drosophilidae; Drosophila.

E l (bases 1 to 670)

Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E.,

Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V.,

Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N.,

Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunoo, J.,

Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C.,

Bugp/HHM AT Drosophila EST Project

Unpublished (2000)
                                                                                                                                                                                                                                         988 ACAAGATCCAGGAAAGCCAGTCGATTCCCAATCCGATTGTCAGCAGCAATAGCGTGAATA 1047
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AT.121-AT.1319: DH5-alpha TonA"
AT.121-AT.1319: DH5-alpha TonA"
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/note="Organ: ADULT testes; Vector: pOTB7; Site_1: EcoR1;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library."
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BG634444
BG634444
BG63455prime AT Drosophila melanogaster adult testes pOTB7
BC63650bila melanogaster cDNA clone AT30655 5 similar to CG1453:
FBan0001453 'motor protein' located on: X 10A6-10A7;: 04/09/2001,
                                                        421 TAGAACTGGACGCCATACTCACGCTCAATCCGGAGCTAATGCAAGATACTGTCGAACAGC
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One Cyclotron Rd, Berkeley, CA 94720, USA
Pax: 510 486 (49.98
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003485: arm:X [10878159,11180508]
estimated-cyto:10A3-10B11: 04/09/2001
Plate: AT.306 row: E column: 7
High quality sequence stop: 615.
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/organism="Drosophila melanogaster"
/mol_type="mRNA"
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BG634444.1 GI:13761981
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/lab host="Plates AT.10-AT.120: DH5-alpha. Plates
AT.121-AT.1319: DH5-alpha TonA"
/clone lib="AT Drosophila melanogaster adult testes pOTB7"
/clone lib="AT Drosophila melanogaster adult testes pOTB7"
/note="Organ: ADULT testes; Vector: pOTB7; Site 1: RCOR1;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into pOTB7. Plasmid cDNA library."
1 (bases 1 to 679)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E.,
Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V.,
Farfan, D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N.,
Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J.,
Lewis, S. E., Cellniker, S. and Rubin, G.M.
BDGP/HHMI AT Drosophila EST Project
Unpublished (2000)
Con Dec 6, 2000 this sequence version replaced gi:11578538.
Contact: Stapleton, M.
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                                                                                                                                                                                                                                                                      Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003485: arm:X [10878159,11180508]
estimated-cyto:10A3-10B11: 04/07/2001
Plate: AT.41 row: B column: 2
High quality sequence stop: 655.
Location/Qualifiers
1. 679
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Pred. No. 3.2e-161;
0; Mismatches 7;
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/clone="AT04114"
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Rubin,G.M. TITLE BDGP/HHMI RH Drosophila EST Project JOURNAL Unpublished (2001) COMMENT Contact: Stapleton, M. BDGP Lawrence Berkeley National Lab One Cyclotron Rd, Berkeley, CA 94720, USA FAX: 510 486 6798 Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu hit genomic AE003485: arm:X [10878159,11180508] estimated-cyrc.10A3-10B11: 08/17/2001 Plate: RH.145 row: E column: 8 High quality sequence stop: 563. Location/Qualifiers source /organism="Drosophila melanogaster" /mol type="mRNA" /db xref="taxon:7227" /clone="RH14556" /sex="male and female" /do stage="Adult" /lab host="Mill Prosophila melanogaster normalized Head pRice-1" /nore-"program: head. Vortor: nplc1: Site 1: Xhor: Site 2: /nore-"program: head. Vortor: nplc1: Site 2: /nore-"program: head. Nortor: nplc1: Site 2: /nore-"program: head. Nortor: nplc1: Site 2: /nore-"program: head. Nortor: nplc1: Nplc2: Head. Nplc2: Nplc2: Nplc2: Nplc2: Npl	/ Notes - Organ: nead; vector: price; stee 1: Anol; site = Lambin. Library was kindly generated by Piero Carninoi the RIKEN. The library was normalized and excised usi Cre recombinase. Plasmid cDNA library." IGIN Query Match 21.5%; Score 662.4; DB 3; Length 664; Best Local Similarity 99.8%; Pred. No. 7.4e-161; Matches 663; Conservative 0; Mismatches 1; Indels 0; Gaps	1 1 1 1 1 1 1 1 1 1	
Best Local Similarity 99.4%; Pred. No. 3.6e-161; Matches 666; Conservative 0; Mismatches 4; Indels 0; Gaps 0; O; O; O; O; O; O; O;	Db 301 TGGGGCGTCAAGCGTCAAGCGGCGCGCGCCCCCCCCCCTCTCTCT	481 TGGAACGCCCCCGGAGCCCAAGAACCAGCGCCGATGAACCTCTCGC 919 GTAATCCCACACACCCCCGGAGCCCAAGAACCAGCCGCGCCGATGAACCTCTCGC 919 GTAATCCCACAACAATCGGCTATCGGTGGCAATCTCACCAGCCGTATGACCATGGCCGGAA 541 GTAATCCCACACAACCGGTGGCAATCTCACCAGCCGTATGACCATGGCCGGAA 979 ACATGCTGAACACAACCCAGCAAGCCAGTCGATTCCCAATCCGATTGTCAGCAGCAATA 1039 GCGTGAATA 1048 1039 GCGTGAATA 1048 661 GCTTGAATAC 670	REBULT 15 B1609735 LOCUS B1609735 B1609736 B16097374 B16097374 B16097374 B1609736 B16097374 B1609774 B16097374 B16097374 B16097374 B16097374 B16097374 B1609736 B1609

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